User Guide: Imaging

Horizontal and Micro NMR Imaging
With VNMR 6.1C Software

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VARIAN

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Imaging modules on Varian NMR superconducting spectrometer systems with VnmrIMAGE version 4.4 software installed.

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SAFETY PRECAUTIONS

The following warning and caution notices illustrate the style used in Varian manuals for safety precaution notices and explain when each type is used:

WARNING: ***Warnings*** **are used when failure to observe instructions or precautions could result in injury or death to humans or animals, or significant property damage.**

CAUTION: ***Cautions*** **are used when failure to observe instructions could result in serious damage to equipment or loss of data.**

Warning Notices

Observe the following precautions during installation, operation, maintenance, and repair of the instrument. Failure to comply with these warnings, or with specific warnings elsewhere in Varian manuals, violates safety standards of design, manufacturing, and intended use of the instrument. Varian assumes no liability for customer failure to comply with these precautions.

WARNING: **Persons with implanted or attached medical devices such as pacemakers and prosthetic parts must remain outside the 5-gauss perimeter from the centerline of the magnet.**

The superconducting magnet system generates strong magnetic fields that can affect operation of some cardiac pacemakers or harm implanted or attached devices such as prosthetic parts and metal blood vessel clips and clamps.

Pacemaker wearers should consult the user manual provided by the pacemaker manufacturer or contact the pacemaker manufacturer to determine the effect on a specific pacemaker. Pacemaker wearers should also always notify their physician and discuss the health risks of being in proximity to magnetic fields. Wearers of metal prosthetics and implants should contact their physician to determine if a danger exists.

Refer to the manuals supplied with the magnet for the size of a typical 5-gauss stray field. This gauss level should be checked after the magnet is installed.

WARNING: **Keep metal objects outside the 10-gauss perimeter from the centerline of the magnet.**

The strong magnetic field surrounding the magnet attracts objects containing steel, iron, or other ferromagnetic materials, which includes most ordinary tools, electronic equipment, compressed gas cylinders, steel chairs, and steel carts. Unless restrained, such objects can suddenly fly towards the magnet, causing possible personal injury and extensive damage to the probe, dewar, and superconducting solenoid. The greater the mass of the object, the more the magnet attracts the object.

Only nonferromagnetic materials—plastics, aluminum, wood, nonmagnetic stainless steel, etc.—should be used in the area around the magnet. If an object is stuck to the magnet surface and cannot easily be removed by hand, contact Varian service for assistance.

Warning Notices (*continued*)

Refer to the manuals supplied with the magnet for the size of a typical 10-gauss stray field. This gauss level should be checked after the magnet is installed.

WARNING: **Only qualified maintenance personnel shall remove equipment covers or make internal adjustments.**

Dangerous high voltages that can kill or injure exist inside the instrument. Before working inside a cabinet, turn off the main system power switch located on the back of the console, then disconnect the ac power cord.

WARNING: **Do not substitute parts or modify the instrument.**

Any unauthorized modification could injure personnel or damage equipment and potentially terminate the warranty agreements and/or service contract. Written authorization approved by a Varian, Inc. product manager is required to implement any changes to the hardware of a Varian NMR spectrometer. Maintain safety features by referring system service to a Varian service office.

WARNING: **Do not operate in the presence of flammable gases or fumes.**

Operation with flammable gases or fumes present creates the risk of injury or death from toxic fumes, explosion, or fire.

WARNING: **Leave area immediately in the event of a magnet quench.**

If the magnet dewar should quench (sudden appearance of gasses from the top of the dewar), leave the area immediately. Sudden release of helium or nitrogen gases can rapidly displace oxygen in an enclosed space creating a possibility of asphyxiation. Do not return until the oxygen level returns to normal.

WARNING: **Avoid liquid helium or nitrogen contact with any part of the body.**

In contact with the body, liquid helium and nitrogen can cause an injury similar to a burn. Never place your head over the helium and nitrogen exit tubes on top of the magnet. If liquid helium or nitrogen contacts the body, seek immediate medical attention, especially if the skin is blistered or the eyes are affected.

WARNING: **Do not look down the upper barrel.**

Unless the probe is removed from the magnet, never look down the upper barrel. You could be injured by the sample tube as it ejects pneumatically from the probe.

WARNING: **Do not exceed the boiling or freezing point of a sample during variable temperature experiments.**

A sample tube subjected to a change in temperature can build up excessive pressure, which can break the sample tube glass and cause injury by flying glass and toxic materials. To avoid this hazard, establish the freezing and boiling point of a sample before doing a variable temperature experiment.

Warning Notices (*continued*)

WARNING: **Support the magnet and prevent it from tipping over.**

The magnet dewar has a high center of gravity and could tip over in an earthquake or after being struck by a large object, injuring personnel and causing sudden, dangerous release of nitrogen and helium gasses from the dewar. Therefore, the magnet must be supported by at least one of two methods: with ropes suspended from the ceiling or with the antivibration legs bolted to the floor. Refer to the *Installation Planning Manual* for details.

WARNING: **Do not remove the relief valves on the vent tubes.**

The relief valves prevent air from entering the nitrogen and helium vent tubes. Air that enters the magnet contains moisture that can freeze, causing blockage of the vent tubes and possibly extensive damage to the magnet. It could also cause a sudden dangerous release of nitrogen and helium gases from the dewar. Except when transferring nitrogen or helium, be certain that the relief valves are secured on the vent tubes.

WARNING: **On magnets with removable quench tubes, keep the tubes in place except during helium servicing.**

On Varian 200- and 300-MHz 54-mm magnets only, the dewar includes removable helium vent tubes. If the magnet dewar should quench (sudden appearance of gases from the top of the dewar) and the vent tubes are not in place, the helium gas would be partially vented sideways, possibly injuring the skin and eyes of personnel beside the magnet. During helium servicing, when the tubes must be removed, carefully follow the instructions and safety precautions given in the manual supplied with the magnet.

Caution Notices

Observe the following precautions during installation, operation, maintenance, and repair of the instrument. Failure to comply with these cautions, or with specific cautions elsewhere in Varian manuals, violates safety standards of design, manufacturing, and intended use of the instrument. Varian assumes no liability for customer failure to comply with these precautions.

CAUTION: **Keep magnetic media, ATM and credit cards, and watches outside the 5-gauss perimeter from the centerline of the magnet.**

The strong magnetic field surrounding a superconducting magnet can erase magnetic media such as floppy disks and tapes. The field can also damage the strip of magnetic media found on credit cards, automatic teller machine (ATM) cards, and similar plastic cards. Many wrist and pocket watches are also susceptible to damage from intense magnetism.

Refer to the manuals supplied with the magnet for the size of a typical 5-gauss stray field. This gauss level should be checked after the magnet is installed.

Caution Notices (*continued*)

CAUTION: **Keep the PCs, (including the LC STAR workstation) beyond the 5-gauss perimeter of the magnet.**

Avoid equipment damage or data loss by keeping PCs (including the LC workstation PC) well away from the magnet. Generally, keep the PC beyond the 5-gauss perimeter of the magnet. Refer to the *Installation Planning Guide* for magnet field plots.

CAUTION: **Check helium and nitrogen gas flowmeters daily.**

Record the readings to establish the operating level. The readings will vary somewhat because of changes in barometric pressure from weather fronts. If the readings for either gas should change abruptly, contact qualified maintenance personnel. Failure to correct the cause of abnormal readings could result in extensive equipment damage.

CAUTION: **Never operate solids high-power amplifiers with liquids probes.**

On systems with solids high-power amplifiers, never operate the amplifiers with a liquids probe. The high power available from these amplifiers will destroy liquids probes. Use the appropriate high-power probe with the high-power amplifier.

CAUTION: **Take electrostatic discharge (ESD) precautions to avoid damage to sensitive electronic components.**

Wear a grounded antistatic wristband or equivalent before touching any parts inside the doors and covers of the spectrometer system. Also, take ESD precautions when working near the exposed cable connectors on the back of the console.

Radio-Frequency Emission Regulations

The covers on the instrument form a barrier to radio-frequency (rf) energy. Removing any of the covers or modifying the instrument may lead to increased susceptibility to rf interference within the instrument and may increase the rf energy transmitted by the instrument in violation of regulations covering rf emissions. It is the operator’s responsibility to maintain the instrument in a condition that does not violate rf emission requirements.

Introduction

This manual describes the parameters, macros, pulse sequences, and general operating procedures used for imaging and localized spectroscopy experiments on Varian NMR spectrometers using VNMR version 6.1C. The primary purpose of this manual is to document the Varian VnmrIMAGE advanced applications interface. The manual contains the following chapters:

- Chapter 1, "First Steps: Making an Image,"introduces you to the typical steps in setting up and running a VnmrIMAGE pulse sequence.
- Chapter 2, "Imaging Experiments,"describes the basic concepts necessary to understand MRI experiments.
- Chapter 3, "Imaging Pulse Sequences,"describes some of the pulse sequences for imaging available in Varian NMR spectrometers.
- Chapter 4, "Image Browser," covers ImageBrowser, a comprehensive image viewing and analysis program.
- Chapter 5, "Image Browser Math Processing,"describes ImageBrowser, which is used in conjunction with Image Browser to do more complex processing.
- Chapter 6, "CSI Data Processing,"describes a tool for easy processing of chemical shift image data (CSI).
- Chapter 7, "High-Performance Auxiliary and Microimaging Gradients," covers the high-performance auxiliary gradient (HPAG) accessory.
- Chapter 8, "Digital Eddy Current Compensation," describes the function of the Digital Eddy Current Compensation module and the associated software interface, `decctool`
- Chapter 9, "Physiological Gating Module," explains how to use the physiological gating module (PGM), which detects the ECG of the experimental subject and sends a trigger pulse to the spectrometer for prospective gating experiments.
- Chapter 10, "2D and 3D Backprojection,"shows how to acquire and reconstruct 2D and 3D NMR images based on the backprojection (BP) or projection reconstruction.

An appendix lists VNMR commands, macros, and parameters used commonly for imaging and localized spectroscopy experiments.

VnmrIMAGE Interface

Many new features and capabilities have been introduced with the VnmrIMAGE interface. The underlying philosophy of the software is to promote a friendly and convenient applications environment and improve the ease-of-use tools available within VNMR. VnmrIMAGE highlights include:

- Automated setup and optimization of imaging gradients.
- RF calibration database for automatic selection of pulse power levels.
- Expanded pulse sequence library and pulse sequence programming capabilities, including oblique angle imaging.
- Graphical planning of imaging and localized spectroscopy experiments.

Software Compatibility

The new software described in this manual is designed to be compatible with already existing software. Older style pulse sequences and macros, both SISCO-supplied and user-written, should continue to work as they always have. We have consciously avoided names for pulse sequences and macros that have long-standing definitions, even though this sometimes meant creating new names that are perhaps slightly less descriptive. The definitions of some parameters have changed, but older parameter sets will continue to function properly with their corresponding pulse sequences. Older sequences and their respective parameter sets, such as IMAGE and SSFP, will continue to work properly when used with the proper macros, but you need to take care not to “mix and match” old and new.

Notational Conventions

The following notational conventions are used throughout all VNMR manuals:

- Typewriter-like characters identify VNMR and UNIX commands, parameters, directories, and file names in the text of the manual. For example:
  The `shutdown` command is in the `/etc` directory.
- The same type of characters show text displayed on the screen, including the text echoed on the screen as you enter commands during a procedure. For example:
  `Self test completed successfully.`
- Text shown between angled brackets in a syntax entry is optional. For example, if the syntax is `seqgen s2pul<.c>`, entering the “`.c`” suffix is optional, and typing `seqgen s2pul.c` or `seqgen s2pul` is functionally the same.
- Lines of text containing command syntax, examples of statements, source code, and similar material are often too long to fit the width of the page. To show that a line of text had to be broken to fit into the manual, the line is cut at a convenient point (such as at a comma near the right edge of the column), a backslash (\) is inserted at the cut, and the line is continued as the next line of text. This notation will be familiar to C programmers. Note that the backslash is not part of the line and, except for C source code, should not be typed when entering the line.
- Because pressing the Return key is required at the end of almost every command or line of text you type on the keyboard, use of the Return key will be mentioned only in cases where it is *not* used. This convention avoids repeating the instruction “press the Return key” throughout most of this manual.
- Text with a change bar (like this paragraph) identifies material new to VNMR that was not in the previous version of VNMR. Refer to the *VNMR Release Notes* for a description of new features to the software.

Purpose of This Manual

This manual should instruct both new and experienced SISCO users. If you are a new user, this should be your reference for imaging and localized spectroscopy applications. Because we want to spare new users the duplication of effort required to learn both old and new, we have explicitly left out references to the older methods in most of this manual. Other VNMR manuals you will find useful include:

- *VNMR Command and Parameter Reference*
- *VNMR User Programming*
- *VNMR and Solaris Software Installation*

Chapter 1. First Steps: Making an Image

Sections in this chapter:

This chapter describes the typical steps in setting up and running a VnmrIMAGE pulse sequence. The SEMS (Spin-Echo Multislice) pulse sequence is used as an example. If you have been running the IMAGE, MSLICER, or SHORTE sequences, this is a direct replacement.

We assume that a probe and sample are in place, the probe is tuned properly, and that the system is otherwise ready to run. If you are running the system for the first time and need instructions on setting up or turning on any of the hardware, you should refer to the manual *Getting Started*.

Most of the macros used for imaging are located in the subdirectory `maclib.imaging` of `/vnmr/maclib`. Similarly, menus used for imaging are placed in the subdirectory `menulib.imaging` of `/vnmr/menulib`. The system knows that you want access to these imaging subdirectories through the value of the parameter `appmode`, a global parameter that each user can set.

To set the value of `appmode` for imaging:

- Enter **`appmode='imaging'`** on the VNMR command line.

  Alternatively, you can select Setup from the Main menu, select App Mode, and then select Imaging.

This sets global parameters `sysmaclibpath` and `sysmenulibpath` to the path of the following imaging directories so that these directories are searched each time you enter a command:

- `sysmaclibpath` is set to `'/vnmr/maclib/maclib.imaging'`
- `sysmenulibpath` is set to `'/vnmr/menulib/menulib.imaging'`

For more information about the commands, parameters, and procedures used, refer to the appropriate chapters elsewhere in this manual and to the *VNMR Command and Parameter Reference*.

1.1 Making an Initial Scout Image

The following procedures outline all of the steps you need to take to begin using SEMS for the first time. Some of the steps, such as pulse calibration, may not be necessary once you have done them once. It is likely that in a real experimental session you may go through two or more stages in defining the image orientation and position for the area of interest. We call this final image the “target” image. But first, you will probably need to acquire an initial “scout” image that can be used to accurately locate the target image.

Calibrating the Pulse Length

The first step is to calibrate the 90° pulse performance of the particular combination of probe and sample, and to enter that information into the `pulsecal` database file:

- Use a simple pulse-acquire sequence (e.g, S2PUL), set the power level to intermediate range (on newer UNITY*INOVA* or UNITY*plus* systems, set `tpwr` to about `50`; on UNITY or VXR-S systems, set `tpwr` closer to `90`).
- Determine either the 90° or 180° pulse length (either value works for this procedure, but a 180 is easier to determine and is generally not distorted by T_1 relaxation).

Now, make an entry in the `pulsecal` file, as follows:

1. Enter the command **`pulsecal`**.

   If you have an entry in `pulsecal`, a table appears in the text window and the following syntax message appears:

   `Usage: pulsecal(name,pattern,length,flip,power)`

   If you have not already made an entry in `pulsecal`, this message appears:

   `pulsecal file does not exist.`

2. Enter **`pulsecal`** again, this time supplying values for the arguments:

   - For `name`, choose a name that makes sense for the probe and/or sample you are using (if this is the cube phantom in the large imaging coil, for example, `'liccube'` might make it easier to select the best entry again if you use this combination at a later date).
   - For `pattern`, unless you used a shaped pulse, enter **`'square'`**. If you used a shaped pulse, enter its name instead.
   - For `length`, enter the pulse length, in μs.
   - For `flip`, if it is a 90° pulse, enter **`90`**, if it is a 180° pulse, enter **`180`**, or whatever value is appropriate.
   - For `power`, enter a value in `tpwr` units used to measure this pulse length.

   For example, if you measured a 180° pulse length of 800 μs with a `tpwr` of 80, your entry is probably `pulsecal('lic','square',800,180,80)`.

   A listing of the new or updated `pulsecal` file is displayed in the text window. The current date (month, day, year) is also included.

Determining the Reference Offset Frequency

You must provide the proton resonance offset frequency for an imaging experiment. You can do this easily now while you have a proton spectrum readily available:

1. Display one of the spectra in the array, for example, `ds(1)`.
2. Set the cursor on the resonance (probably water).
3. Enter the command **`offset`**.

   Record the number that appears in the message window.

Retrieving the Parameter Set

Next, you must retrieve the parameter set to run the SEMS sequence.

1. Join an available experiment. For example, to join experiment 6, enter **`jexp6`**.

2. Retrieve the SEMS parameter set by entering the command **`sems`**.

   You can also use the Files menu system to change to the system `parlib` directory and load in the `SEMS.PAR` parameter set.

Most of the parameters that you need to know about and work with should now be displayed. A few may require being set or selected, but the rest are computed for you.

Setting the rfcoil Parameter

The pulse calibration information, determined in "Calibrating the Pulse Length," page 18, is communicated to the system through the `rfcoil` parameter. The automated setup routines use `rfcoil` to obtain information about probe performance from `pulsecal` and to set pulse powers for the two rf pulses in SEMS.

- Set **`rfcoil='lic'`** (or use whatever name you chose for the `pulsecal` entry).

Setting the gcoil Parameter

An imaging spectrometer is often equipped with multiple gradient sets, which can be interchanged for different sample sizes and experimental requirements. When a new gradient set is introduced into the lab, a corresponding new calibration entry is required in the directory `/vnmr/imaging/gradtables`. Such a calibration file should have been created for any gradient set provided at initial system installation, so first check in the `gradtables` directory for an entry appropriate for your system.

Because a gradient calibration file is a text file containing the maximum gradient strength, rise time, and usable bore size for the gradient coil, a new file can be created manually with any text editor or, most easily, with the macro `creategtable`, as follows:

1. On the VNMR command line, enter the command **`creategtable`**.

   The following prompt appears:

   ```
   Are all gradient axis calibrated to the same maximum
   value? y/n
   ```

2. If you respond `y`, you are asked to give a name to the file. Respond with:
   - The letter `m` for a "main" gradient coil file name.
   - The letter `h` for an "hpag" file name.
   - The letter `o` if you want to define another name. If you respond with `o`, you are asked to enter a name.

3. Enter a brief description of the gradient coil to help in identifying this `gradtables` entry in the future; for example,:

   ```
   Main Actively Shielded Gradient
   ```

4. Enter the usable bore size, in cm, for this gradient set. This value is used only as an internal check of reasonableness for the field of view.

5. Enter the maximum gradient strength, in gauss/cm, for the gradient set.

6. Enter the rise time, in µs. Remember that Varian gradient hardware is installed with a linear slew-rate limitation that is dependent on the gradient set.

The new gradient calibration is now ready to use, but first the configuration parameter `sysgcoil` must be updated to reflect the hardware status.

1. Enter the command **`setgcoil(`*`file`*`)`**, where *`file`* is the appropriate `gradtables` file name, for example, `setgcoil('asg33')`.

This has the effect of setting sysgcoil to the same file name, but in this special case, it also updates the configuration file as well.

2. As new parameter sets are retrieved, and as other experiments are joined, the system updates gradient calibration parameters to new values. To verify this, enter **gmax?** and **trise?** to see that they have the correct values for your gradient hardware.

Note that gmax and trise are updated when a new parameter set is loaded, or when you join a different experiment. One exception is joining an experiment that has gcoil parameter set to the value of sysgcoil. If you update the gradient calibration parameters of an already existing entry in gradtable, you must manually update gmax and trise in the current experiment and others that have gcoil set to the sysgcoil value, or run the macro _gcoil in each case.

Setting the pilot Parameter

Some SEMS parameter sets might have not set the pilot parameter. To ensure that all of the refocusing parameters are properly computed within the pulse sequence:

- Set **pilot='y'**

Setting the resto Parameter

The value of the resto parameter is used to make sure all positions are properly referenced to the center of the magnet and gradients.

- Set **resto** to the value you found in "Determining the Reference Offset Frequency," page 18.

Setting the Field-of-View Parameters

Choose values for the image field-of-view (FOV) and enter them as follows:

1. Set **lro** to the readout length, in cm.
2. Set **lpe** to the phase encode length, in cm.

Do not use the old macros setgro and setgpe.

Setting the Slice Thickness

The parameter thk sets the slice thickness for an image.

- Set **thk** to the slice thickness, in mm. A value of 2 or 3 is a good place to start.

Selecting the Image Orientation

The parameter orient defines the imaging slice plane and indirectly controls a set of three Euler angle parameters that the pulse sequence uses internally to achieve the desired orientation. orient has allowed values of 'trans', 'sag', and 'cor', short for transverse (Z slice gradient), sagittal (X slice gradient), and coronal (Y slice gradient), respectively. A fourth entry of 'oblique' is also possible, but cannot be entered directly. The entry for orient in the appendix (see page 324) describes oblique slice selection.

Because it is common for the sample to be fairly well centered on the X axis, even if it is off center in Y and Z, you might start by entering **orient='sag'**. For a vertical bore

magnet, Z is more likely to be the on-center axis, so enter **orient='trans'**. This nearly guarantees that you will slice through the sample without having to hunt around.

- Set `orient` to `'trans'`, `'sag'`, or `'cor'`, as appropriate.

Setting the pss Parameter

Parameter `pss` determines the slice position relative to the gradient origin. Setting `pss` automatically sets the related parameter `ns`, the number of slices. You cannot set `ns` directly, but entering an array of slice positions into `pss` results in an update of `ns` to the proper value determined by the size of the `pss` array.

- Set `pss` as an array of slice positions, in cm, relative to the gradient origin (you probably want to set `pss=0`).

Checking the seqcon Parameter

Some early SEMS parameter sets may have set the `seqcon` parameter to an incorrect (although valid) setting. See "Acquisition Loop Control" on page 338 for more information on this parameter. For proper multislice operation in SEMS:

- Check that `seqcon='ncsnn'`. Update it to this value if necessary.

Selecting Values for the tr and te Parameters

You may want to change the default values of `tr` and `te`. Keep in mind that unlike `d1` in the old IMAGE sequence, `tr` is now the correct measure of the total repetition time for a multislice experiment (i.e., the time between successive excitations of one slice).

- If desired, set `tr` and `te` to new values, in seconds.

Entering the imprep Command

Everything necessary to set up an image is now done. To proceed:.

1. Enter the command **imprep**.

   This command takes the information about your rf coil, the slice thickness and field of view you have selected, and computes and sets the parameters `gro`, `gpe`, `gss`, `tpwr1`, `tpwr2`, and `sw`.

2. If the parameter `nv` was zero, a warning is issued; otherwise, `nv` is left alone, so if you want just a projection, first set `nv` to zero (`nv` controls the number of phase-encode steps, and is described in more detail on page 335) and ignore the warning.

3. You should get the message "`setup complete`" if all went well. If not, you should get an error message that gives you some hint of what could be wrong.

Checking the Readout Projection

It is a good idea to get a zero phase-encode projection to check proper operation and to center the image in the readout direction.

1. Enter **nv=0** to specify just the projection, then enter **ga** to run the experiment.

2. If the resulting projection is off-center, put the cursor where you want the new center to be and enter **movepro**, which computes a new value for the `pro` (readout position) parameter. `pro` sets the proper frequency during data acquisition.

Entering the go Command

The final step is to complete the image and see the end product.

1. If you are making a projection with `nv=0`, enter **`ga`**; otherwise, for the complete image, set `nv` to the number of phase encode increments you want (typically 128 or 256) and enter **`go`** (the difference is that `ga` automatically does a 1D transform of every data line, which we don't want, and `go` doesn't).
2. When the image is complete, enter **`ft2d`** to see the result.

Uncommonly Used Parameters

Although there is nearly a complete overlap in software between Varian's horizontal imaging, vertical microimaging, and standard analytical NMR systems, there are a few parameters that are not normally used on a horizontal bore system. If set incorrectly, these parameters can lead to artifacts or positional errors in images. It is therefore useful to check the following parameters on horizontal bore imaging machines. Users with previous experience with the SISCO 93.1 version of VNMR software are particularly advised to learn about these parameters, because they did not exist in version 93.1.

`load` Determines how shim values are updated, i.e., if they are obtained from the software settings in the current experiment or from the actual existing hardware settings. Most Varian users are familiar with this, but SISCO users new to Varian software should refer to the *VNMR Command and Parameter Reference* for more information.

`solvent` Used to fine tune the spectrometer frequency to compensate for the small reference field shifts caused by deuterium locking to different solvents. Because most imaging experiments are performed without deuterium lock, it is a good idea to set `solvent='none'` in all experiments, including S2PUL, for consistent frequency settings. Failure to do this results in an incorrectly referenced `resto` parameter, which in turn could result in positional errors in images.

`homo` Enables time-shared homonuclear decoupling and should generally be set to `'n'` for imaging experiments.

1.2 Using the Scout Image to Plan a New Target Image

Now that you have acquired the first scout image, let's use it to locate a new target image that it includes whatever features you are interested in observing. You can skip many of the steps we had to go through to get the scout, such as rf calibration, determination of `resto`, etc., because these do not change from the scout to the new target image.

Moving the Parameters to New Experiment

You need to copy the parameter set you have been working with to another experiment (the "target" experiment). You do not have to do this as the first step, but you need do it eventually, so let's get it out of the way. It is possible to both plan and acquire the target image in the same experiment, but then the scout image is lost, which we might want to use again to plan a different target.

- To make the copy, enter **`mp(new_exp)`**. This moves the entire imaging parameter set to the designated experiment. For purposes of this example and the rest of this chapter,

assume that you have been working in experiment 2 to acquire the scout image and wish to use experiment 6 to acquire the target image. In this case, enter **`mp(6)`**.

Starting the Planning Session

To start planning:

1. Enter the command **`plan`**.
2. Click on the **Slice** menu button.
3. In the new row of menu buttons, click on **Clear** to remove any previous planning information. The third button is now Mark 1.

Marking the Target Slice Plane

To define a slice plane:

1. Move the cursors to the first point you want to lie in the target image slice plane.
2. Select the **Mark 1** button.
3. Move the cursors to the second point on the line that will define the slice plane.
4. Select **Mark 2**.

You have just selected two points that describe a line through the current scout image. The target image will be perpendicular to the scout slice plane, on the line you have defined. Selecting Compute Target shows this.

If you decide you want to change one or both of the marked points, select Clear again and follow the above procedure once more to define your new slice plane.

If you are working on a system that has gradient waveshaping capabilities, your slice plane may lie at any angle. Slice planes that do not lie along one of the three major axes are said to be *oblique*. If your system does not have gradient waveshaping, the gradient DAC resolution is limited to 12 bits, which is in general not adequate to define arbitrary slice planes with sufficient resolution in readout, phase encode, and slice select directions, and so the software will at this point prevent you from continuing if you have defined a plane that is oblique. (If you want to make sure your two points lie along one of the major axes, here's a hint: Move the cursors to the first point you want to mark; keep the mouse inside the image boundaries but place the mouse arrow outside the blue image box to define the second point. This method causes only one cursor to move and ensures that the two points properly lie along one of the major orthogonal planes).

If you want to define a multislice experiment, you can use the ns and Gap buttons to specify the number of slices and the gap between slices, respectively. When you compute the target slice, the correct slice positions are entered into `pss` automatically. These slice positions are defined in monotonic order, not in interleaved order. But unlike the older imaging sequences, the slice order is not computed inside the sequence, but defined by the array order of `pss`. You can enter the values of `pss` in any order that you like or use the macro `sliceorder` to record slices automatically.

Computing and Displaying the New Target Parameters

At this point, you have specified the target imaging plane or planes on the scout image. You now need to compute the new orientation and slice position for these planes:

- Select the Compute Target button

This button places the results in a set of "target" parameters that will be transferred in the next step to the target experiment. You should see the target Euler angle values printed in the message window, along with the slice position for the line you marked. If you have defined a multislice target, you also see the slice positions displayed in the text window at the bottom of the screen.

The newly defined slice position(s) are drawn over the scout image, allowing you to visually verify that the target image(s) are properly aligned to pass through the desired sample features.

If the new slice position is unsatisfactory, clear it and again perform the procedure (to erase the old slice positions, select Redraw before Compute Target).

Transferring the Target Parameters

The new slice orientation and position parameters can now be communicated to the target experiment. The parameters are the three Euler angles `psi`, `phi`, `theta`, the slice position parameter `pss`, and slice thickness parameter `thk`. The parameter `rfcoil` is also transferred, as well as `resto`, if both experiments have the same `tn`.

1. Select the **Transfer** menu button.

   This button displays a new menu of possible experiment choices and a descriptive listing of each experiment in the text window (this same list can be created at any time with the command `explib2`).

2. Select the experiment to transfer to (in this case Exp 6).

   If there is not enough space to show a menu button for each experiment, you might not see a Current button (transfers internally to the current experiment) or an Other button (enables you to type in an experiment number if the number you want is not displayed).

Because we previously moved parameters from experiment 2 to 6, the target experiment is the same in this case as the scout, except that we are changing the slice position and orientation. We could just as well have transferred the new slice parameters to a completely different imaging experiment (as long as it uses the same parameters to define slice position and orientation).

At this point you are ready to start the new experiment. Because we have not changed the field of view, slice thickness, or rf pulses, there is no need to execute `imprep` again. If you decide to change any of these settings, just make sure you enter **`imprep`** again when everything is adjusted the way you want it.

Checking the FOV and Entering the go Command

Before running the complete target image, it is generally a good idea to make sure that the image is reasonably centered in the readout direction.

1. Set **`nv=0`**, and then enter **`ga`** to get a projection and, if necessary, adjust the cursor and enter **`movepro`**.

2. Set **`nv`** back to the proper number of phase-encode steps, and enter **`go`**.

3. When complete, **`ft2d`** shows you the new target image.

   If you planned a multislice image, you have to set the `cf` parameter to select the slice you want (remember, unlike old imaging sequences, the slices are in the order specified by the `pss` array, and `cf` determines the array index). The macro `dslice` displays up to 12 images at once from a multislice data set.

Chapter 2. Imaging Experiments

Sections in this chapter:

This chapter introduces the basic concepts necessary to understand MRI experiments. You should be familiar with the terminology and principles in simple experiments in conventional NMR because this chapter focuses on MRI-related topics. NMR concepts can be easily understood when the process of a simple imaging experiment is analyzed. The 2D spin-warp imaging sequence that is commonly performed in MRI is used in this chapter as an example to illustrate principles and experimental aspects related to NMR.

The spin-warp imaging sequence is based on the 2D Fourier transform principle for converting the time domain NMR signals into image data. Most of the other imaging techniques are also based on the Fourier transform idea and can be regarded as variations of the spin-warp method.

2.1 Basic Imaging Principles

This section contains a brief introduction to nuclear magnetic resonance imaging (NMRI), magnetic resonance spectroscopy, chemical shift imaging, the 2D spin-warp imaging sequence, and lists several additional references for more information about NMRI.

NMR Imaging

NMR imaging, or MRI, is used to obtain a map of the distribution of spins in a sample (for example, protons in water). The inherent properties of the spins—such as spin density (T_1, T_2, T_2*), diffusion coefficient, etc.—affect the signal intensity in imaging experiments, which makes the contrast in the resulting images easy to distinguish. This feature of distinguishing different sample regions based on NMR-related properties makes imaging an important tool in clinical, biological, and material sciences.

For example, clinical MRI scanning techniques are the preferred method for distinguishing various soft tissues in the body. The spin density (T_1 and T_2) of water in different tissue

regions makes the contrast between tissues easy to distinguish. Experimental techniques can be designed to further enhance the contrast between tissues. Special imaging techniques can also be used to study flow, perfusion, diffusion, and susceptibility effects.

Methods for Obtaining Spectral and Spatial Information

Magnetic resonance spectroscopy (MRS) is the study of spectroscopic information in different spatial regions in a sample. Volume-localized spectroscopic methods are used to obtain spectral information from specific locations in a sample. Chemical shift imaging (CSI) methods are another related class of experiments that are designed to provide both spectral and spatial information from a single experiment.

2D Spin-Warp Imaging Sequence

2D spin-warp imaging is one of the simplest imaging sequences commonly used in NMRI. Most of the other imaging sequences are variations of this fundamental sequence.

In "Basic Imaging Principles," page 25, the basic principles of imaging are discussed based on the spin-warp sequence. The information in that section is primarily meant to help a novice grasp the basic principles and terminology of NMRI. The chapter contains a description of the experimental aspects of NMRI so that you can understand the correlation between the parameters and the resulting image. For a more theoretical understanding of the imaging experiments, refer to any basic text or reviews on MRI.

References

The VNMR manual *Getting Started* contains more general information on operating Varian spectrometers. Consult the manual *VNMR Command and Parameter Reference* for additional information on VNMR commands or parameters.

2.2 Time Domain to Spatial Domain Conversion

As an example of Time domain to spatial domain conversion, consider a tube of water inserted within an NMR probe and placed in the center of the magnet. The magnet produces a homogeneous field in the region surrounding the water sample. A single pulse experiment yields an NMR signal that, on Fourier transformation (FT), produces the frequency spectrum of the sample, as shown in Figure 1.

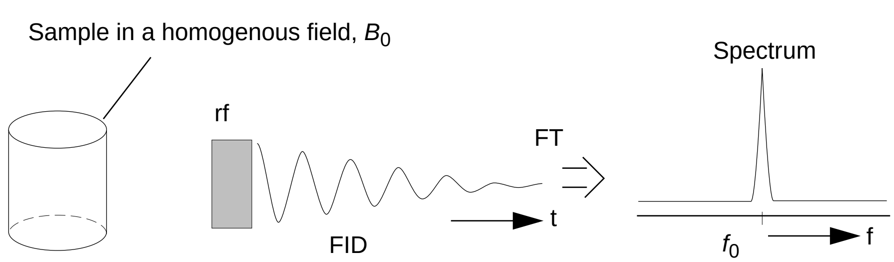


Figure 1. Frequency Spectrum Produced by an NMR Signal

A single line at the resonance frequency, f_0, is obtained. The frequency is defined by the following Larmor equations:

$$f_0 = \gamma' \cdot B_0 \quad \text{[Eq. 1]}$$

$$\gamma = 2\pi \cdot \gamma' \quad \text{[Eq. 2]}$$

In Equation 1 and Equation 2, γ is the gyromagnetic ratio (rad.gauss^{-1}sec^{-1}) and B_0 is the magnetic field strength (gauss).

For protons, γ is 2.6752×10^4 rad.gauss^{-1} sec^{-1} and γ' is 4257 Hz.gauss^{-1}. In MRI, the magnet strength, B_0, is usually expressed in tesla (1 T = 10,000 gauss), whereas in conventional NMR, magnet strength is commonly referred to in terms of the proton resonance frequency in MHz.

The frequency spectrum that is displayed in NMR is referenced with respect to the rf transmitter frequency. The center of the spectrum refers to the carrier frequency. Therefore, spectral components that are above (positive) and below (negative) can be measured by NMR. In MRI, the spatial-frequency components are measured with respect to the resonance frequency of the major component in the sample, usually water. Therefore, the carrier is placed on the water resonance frequency, f_0, as part of the initial setup procedure. Now, the center frequency in the spatial-frequency domain refers to the origin, or the center, of the gradient frame of reference.

In addition to the standard equipment in NMR spectrometers, imaging systems are equipped with *X*, *Y*, and *Z* field gradient coils that are designed to produce linear field gradients along the *x*, *y* and *z* directions, respectively. In MRI, these field gradients are used to get the spatial information from the sample. The *x*, *y*, and *z* gradient fields are orthogonal to each other and their origins lie at the center of the gradient system. The field produced in each direction is linear and ranges from a negative value to a positive value; the field at the origin is zero.

Consider the water sample shown in Figure 1 and apply a linear field gradient along the *y* direction, ranging from a negative value to a positive, as shown in Figure 2.

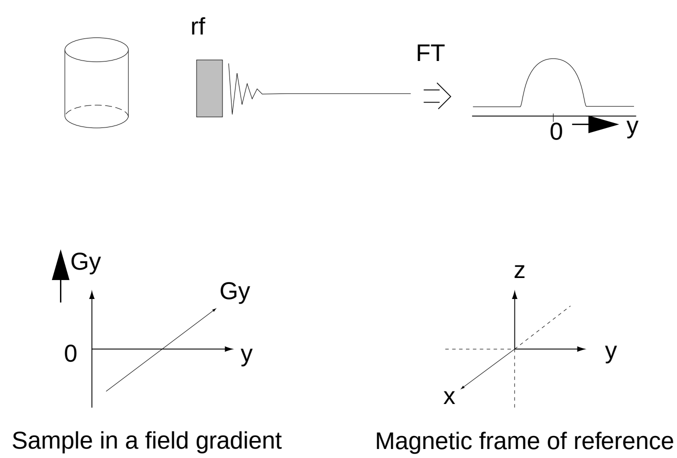


Figure 2. Effect of a Field Gradient Along Direction *y*

In Figure 2, the field along the *y* direction is no longer constant but varies linearly, depending on the position *y*. The field at a particular location, *y*, is defined by *y.Gy*, in which *Gy* (in gauss/cm) refers to the field gradient along *y* direction. Therefore, the spins along the *y* direction experience a unique field depending on the location of the *y* direction.

The frequency, *fy*, of the spins at various *y* locations is defined by the following equation:

$$fy = \gamma' \cdot (B_0 + y \cdot G_y) \quad \text{[Eq. 3]}$$

In this equation, *y* refers to the *y* location (in cm) and *Gy* refers to the applied field gradient (in gauss/cm).

Equation 3 is the most important equation in MRI because it correlates the spatial position of the spins, *y*, to the measured parameter, *fy*. That is, the frequency spectrum measured is a direct reflection of spatial information (along *y*) because, as shown in Equation 4,

$$fy \propto \gamma \quad \text{[Eq. 4]}$$

when *y*=0, Equation 4 is the same as Equation 1 and Equation 2, so the frequency at the origin of our frame of reference is equal to the resonance frequency of water, f_0. It is necessary to place the rf transmitter frequency at f_0 so that images can be spatially referenced with respect to the origin of our reference frame or the center of the magnet.

Under the previously described conditions, a single-pulse sequence yields a spectrum that contains a continuous range of frequencies, as shown in Figure 3.

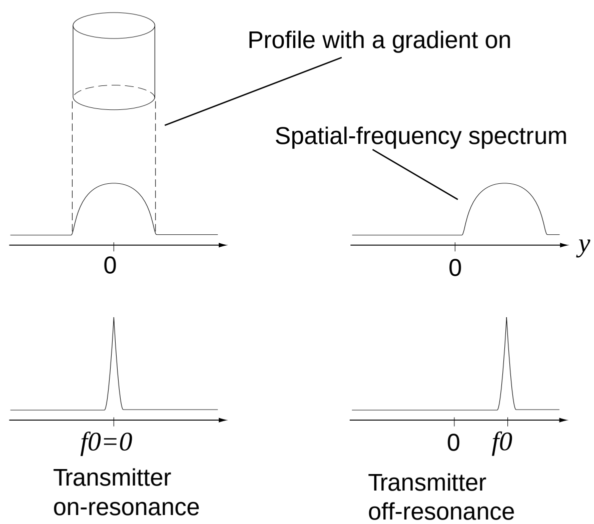


Figure 3. Frequency Ranges

The frequency spread is a direct reflection of the spatial position of the spins along the *y* direction. Signal intensity is directly related to the amount of water at various positions along *y*. The tube of water appears as a semicircle in the center of the spectrum. The *spatial-frequency* spectrum, shown in Figure 3, is also referred to as a *profile* or *projection* of the sample along the *y* direction.

The projection resolves the spatial-frequency components along a single direction. But an imaging sample is three-dimensional, so more imaging must be done to visualize our sample in 3D space. Many experiments have been designed in the past to uniquely identify and map the spin distribution in the sample. Each experiment has its own advantages and limitations. Experiments based on the spin-warp techniques are the most commonly used in MRI. Therefore, it is useful to understand how these experiments resolve the spatial-frequency components of a 3D sample.

The 2D spin-warp experiment contains the following three parts, which correspond to the *preparation*, *evolution*, and *detection* steps in a conventional 2D NMR experiment:

- Slice selection
- Phase encoding
- Readout

2.3 Slice Selection

Magnetic resonance images are displayed as 2D pictures in either grayscale or color scale for further analysis. The 2D images represent the NMR signals taken from a *slice* in the sample, as shown in Figure 4. It is possible to selectively obtain signals from a slice by using a slice-selection process. During the preparation phase of the experiment, only the signals from a predetermined slice are pulsed so that only those excited spins contribute to the resulting image. Slice selection involves using a selective rf pulse in combination with a slice-selection gradient.

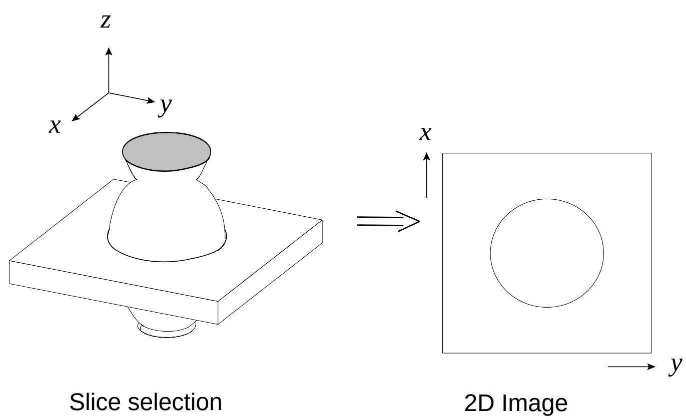


Figure 4. 2D Image Resulting from a Slice Selection

The section "Time Domain to Spatial Domain Conversion," page 26, described how the presence of a field gradient causes a spatial frequency spread (profile) along the gradient direction, shown in Figure 3. In the example shown in Figure 5, the profile along the *z* direction is rectangular because the signal intensities from the sample at various points along z are equal.

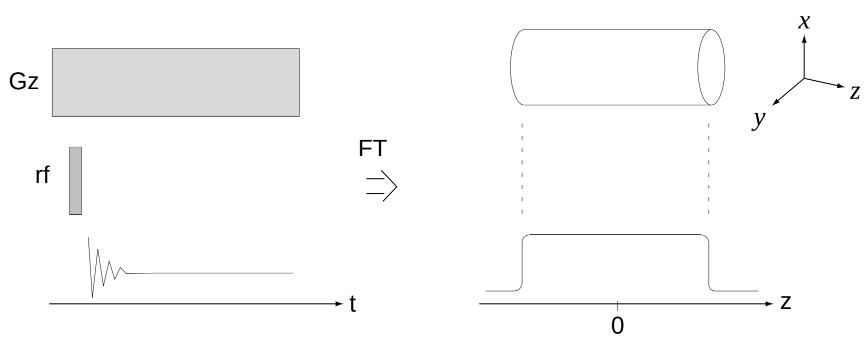


Figure 5. Rectangular Profile

The use of the hard pulse excites all of the spins in the sample because the excitation bandwidth is wider than the frequency spread of the profile. However, if a soft, selective pulse is used, a narrow bandwidth of the profile at the carrier frequency is excited. In other words, spins corresponding to a narrow slice at $z = 0$ are selectively excited. The resulting profile, referred to as the *slice profile*, is shown in Figure 6.

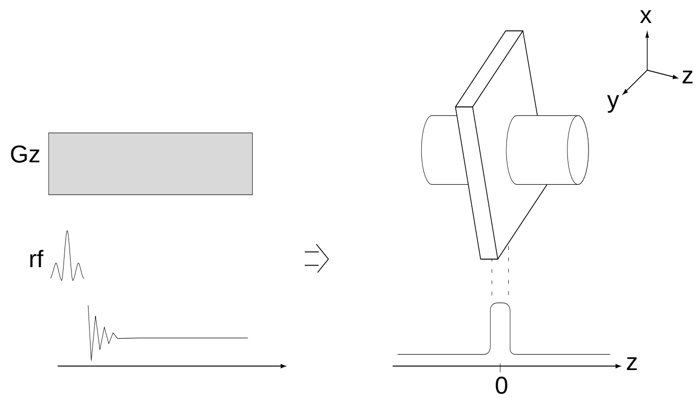


Figure 6. Slice Profile

Ideally, a rectangular slice profile is preferred. A rectangular profile can be achieved by using a shaped pulse with its amplitude modulated in the form of a sinc function, as shown in Equation 5:

$$sin(\theta) / \theta \qquad \text{[Eq. 5]}$$

The phase θ is given in Equation 6:

$$\theta = 2\pi vt \qquad \text{[Eq. 6]}$$

In Equation 6, v is the modulation frequency of the sinc function and t is the time axis.

Theoretically, the resulting excitation profile can be predicted by taking the Fourier transform of the sinc function, which in Equation 5 is rectangular in the frequency domain, as shown in Figure 7.

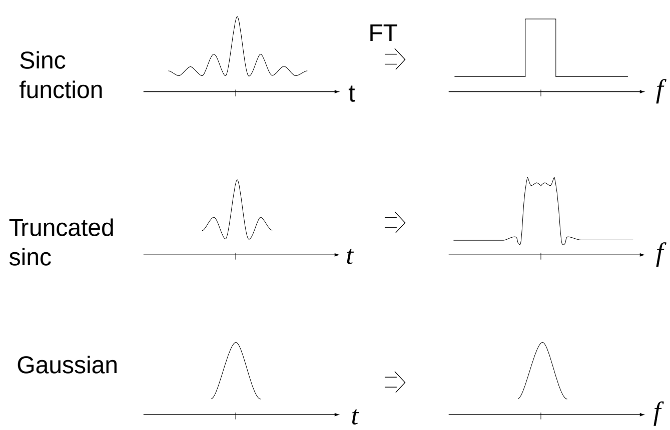


Figure 7. Sinc Function, Truncated Sinc Pulse, and Gaussian-Shaped Slice Profiles

However, in practice, because of experimental limitations such as T_2*, the pulses are limited to about 4 ms or less. The resulting truncated sinc function has an excitation profile, as shown in Figure 7.

Gaussian-shaped pulses are also used for slice-selection purposes. The Gaussian pulse produces a profile that is also a Gaussian, as shown in Figure 7. In general, this simplified approach is only true for short (about 30^{o} or less) flip angles. At larger flip angles, pulses

show large behavior that is not ideal because of the nonlinear response of the NMR spins. The pulse shapes can be optimized to produce more ideal pulse characteristic for specific applications. For example, the rf pulses can be optimized by computer-iterative procedures to give slice profiles that are closer to rectangular shape. Such pulses minimize contamination of the image from regions outside the slice region of interest. The optimization procedures can also produce pulses that are closer to ideal in terms of flip angle and phase response across the slice profile.

So far, we have assumed the transmitter frequency is on-resonance, which corresponds to a slice plane at z = 0. It is also possible to excite a slice at any location along the slice direction by changing the rf transmitter frequency during the excitation phase of the experiment, as shown in Figure 8.

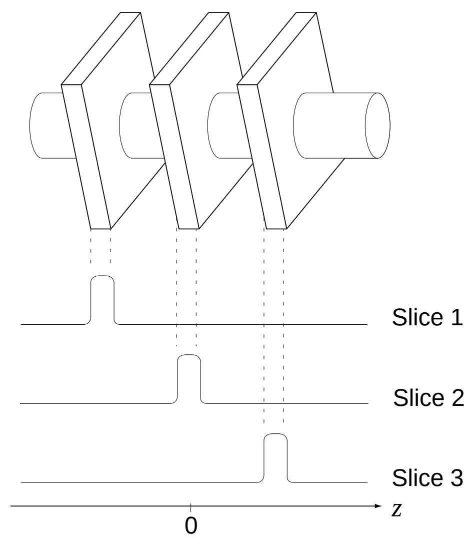


Figure 8. Multislice Excitation

For offset slice selection, the transmitter offset frequency depends on the amplitude of the slice gradient that is applied and is defined by the following equation:

$$(fs - f_0) = \gamma' d \cdot gss \qquad \text{[Eq. 7]}$$

In this equation, *fs* is the transmitter frequency (in Hz) that is needed to excite a slice at distance *d* (in cm) from the origin, f_0 is the resonance frequency (in Hz) of water, and *Gss* is the slice-select gradient (in gauss/cm).

Note: You must return the transmitter reference frequency to the original position during the detection stage of the experiment for proper referencing of the resulting profile.

Slice thickness is directly related to the bandwidth of the excitation pulse. For a sinc pulse, the excitation bandwidth *w* (in Hz) is defined by the following equation:

$$w = 2/\lambda \qquad \text{[Eq. 8]}$$

In Equation 8, λ refers to the wavelength (in sec) of the sinc pulse.

The slice thickness parameter is dependent on the slice gradient because the slice gradient affects the frequency spread or the profile along the slice direction. Equation 9 represents the relationship between the band width of the rf pulse *w* (in Hz), slice gradient *Gss* (in gauss/cm), and slice thickness *st* (in cm).

$$w = \gamma' \cdot Gss \cdot st \qquad \text{[Eq. 9]}$$

The presence of a slice gradient during the slice-selection pulse has an undesirable effect on the signal. The signals lose phase coherence, which results in a rapid signal loss. This signal loss can be restored by applying a gradient of opposite sign, as shown in Figure 9.

The amplitude of the slice rephasing gradient, *Gsd*, can be obtained by the following equation:

$$k \int_{t_7}^{t_4} gss \cdot dt = \int_{t_4}^{t_7} gss \cdot dt \qquad \text{[Eq. 10]}$$

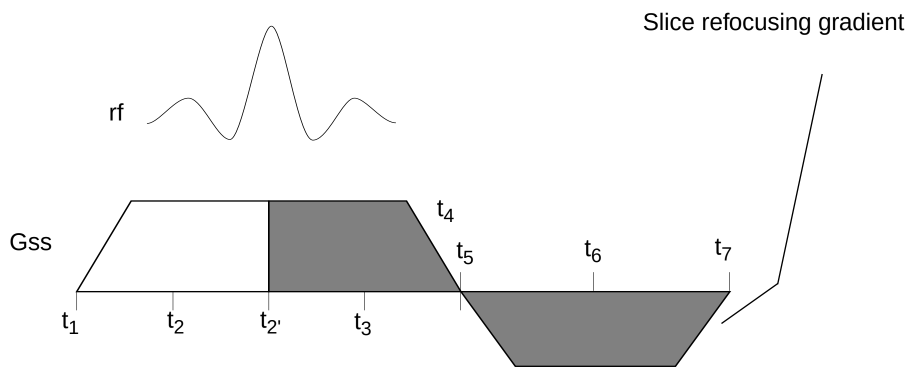


Figure 9. Signal Loss Restoration

In Equation 10, the factor k is approximately equal to 1. Equation 10 simply means that the shaded areas in Figure 9 must be approximately equal for maximum refocusing of the spins after the slice-selection pulse.

Some experimental macros and parameters in VNMR related to slice selection are listed in Table 1. For more information on VNMR macros, parameters, and commands, refer to the manual *VNMR Command and Parameter Reference*.

Table 1. Experimental Macros and Parameters

Macro	*Function*
`plan`	Displays a menu that provides access to the target scan plan utilities. `plan` allows users to define slice positions, offsets `gap`, and the number of slices by using a graphical tool. The parameters can then be transferred to a target experiment using the `transfer` macro.
Parameter	*Function*
`ns`	Sets the number of slices to be acquired for multislice sequences.
`pss`	The position of slice offset, in cm. `pss` is an arrayed parameter; therefore, an arbitrary number of slices can be directly entered. A more convenient way to enter slice offset parameters is to use the `plan` macro.
`resto`	NMR resonance offset frequency, in Hz.
`thk`	The slice thickness, in mm.

2.4 Frequency Encoding

In the presence of a readout gradient, the spatial-frequency components can be directly visualized by observing the profiles along that direction. Even though the presence of a readout gradient during the FID signal gives the necessary information, in practice it is desirable to collect an echo signal. The echo signal, when Fourier transformed, generates only absorption components in the resulting spatial-frequency spectrum or profile. The broad dispersive components are cancelled because of the symmetry of the echo signal.

The cancellation of dispersive components is a big advantage when dealing with imaging data because the image or profile can be generated by simply calculating the absolute value without the need for any phase correction. An echo signal can be generated by first

dephasing the excited spins by using a readout gradient pulse and then rephasing the spins by reversing the sign of the gradient. When the area of the rephasing gradient equals the area of the dephasing gradient, a “gradient echo” is formed, as shown in Figure 10.

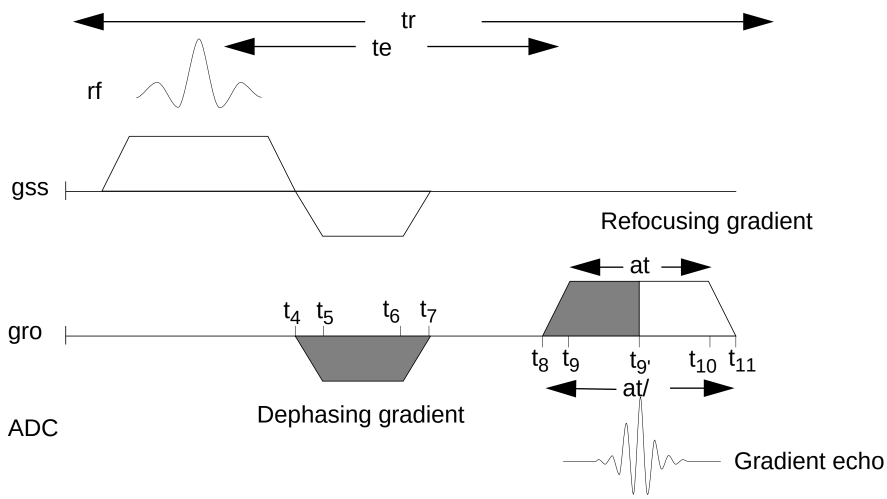


Figure 10. Readout Gradient and Gradient Echo

The readout gradient is applied during the acquisition time, `at`, so that the echo appears at the center of the acquisition window, a condition that is assured if the shaded areas in Figure 10 are equal, as shown in the following equation:

$$\int_{t_3}^{t_4} gro\, dt = \int_{t_5}^{t_6} gro\, dt \qquad \text{[Eq. 11]}$$

The Fourier transform of the echo signal gives the profile along the readout direction; only the signal from the selected slice contributes to the profile. The sequence shown in Figure 10 is commonly used to observe the profile during the initial setup of imaging experiments. The profile can be very useful in doing the following procedures:

- Positioning the sample along the readout direction.
- Checking or calibrating the rf pulse power.
- Setting the receiver gain.
- Checking the signal-to-noise ratio.
- Optimizing the pulse sequence parameters such as `te` and `tr`.

Readout gradient strength determines the frequency spread of image components in a profile. Therefore, the spectral width must be sufficiently wide to resolve all the spatial-frequency components along the readout direction. Otherwise, frequency components outside the spectral window cause “fold-over” artifacts.

The readout gradient and spectral width determine the *field of view* along the readout dimension, defined by the following equation:

$$sw = \gamma' \cdot gro \cdot lro \qquad \text{[Eq. 12]}$$

In Equation 12, `gro` (in gauss/cm) is the readout gradient, `lro` is the field of view along the readout dimension (in cm), and `sw` is the spectral width or bandwidth (in Hz). The spectral width is related to the acquisition parameters, defined by the following equation:

$$sw = (np/2)/at \qquad \text{[Eq. 13]}$$

In Equation 13, `np` is the total number of (real plus imaginary) points digitized, and `at` is the acquisition time (in sec). The maximum bandwidth, `sw`, is determined by the digitizer used on the system. A typical 16-bit digitizer, used on most imaging systems allows a spectral bandwidth limit of 500 KHz, whereas some 12-bit digitizers, used in solids NMR systems, allow a maximum bandwidth of 5 MHz. The parameter `np` is usually set to approximately 128 or 256.

2.5 Phase Encoding

During slice selection (the preparation phase of an experiment), it was possible to restrict the signals to a plane. Spatial-frequency distribution in a plane is achieved by using the evolution (phase encoding) and detection (readout) phases of a 2D NMR experiment. In a spin-warp imaging experiment, a 2D dataset is collected and each orthogonal dimension contains information about the phase encode and readout dimensions, respectively.

Slice selection and frequency encoding (detection phase) are easily visualized by viewing the slice profiles and readout profiles, shown in Figure 5 and Figure 11. The concept of phase encoding is less obvious because information is preserved in the second dimension as a phase modulation. Fourier transformation along the second dimension provides spatial-frequency information. Spatial information corresponding to the phase dimension is encoded by the use of a gradient pulse during phase encoding, as shown in Figure 11.

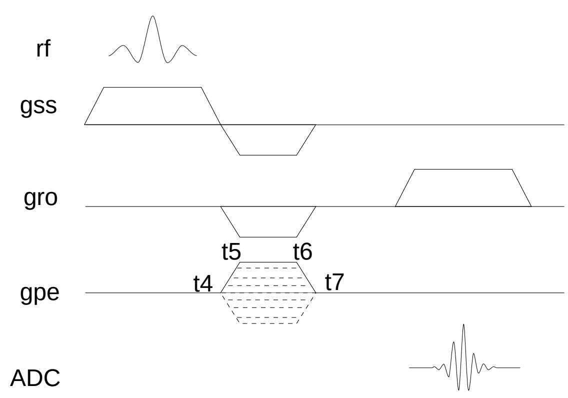


Figure 11. Gradient Echo Imaging Sequence

For example, consider a spin at a specific location, y (in cm), along the phase encode dimension. The phase of the spin, ϕ, is affected by the phase encoding gradient amplitude, `gpe`, and its duration, `tpe`. For an arbitrary pulse, the phase is proportional to the integral area of the gradient pulse, defined by the following equation:

$$\phi = \int_{t4}^{t7} \gamma \cdot y \cdot gpe \cdot dt \qquad \text{[Eq. 14]}$$

In this equation, ϕ is the phase in radians. For a square pulse, Figure 14 reduces to the following expression:

$$\phi = \gamma \cdot y \cdot gpe \cdot tpe \qquad \text{[Eq. 15]}$$

In Equation 15, `tpe` is the phase encode time (in sec).

From Equation 15, it is clear that either tpe or gpe can influence the phase of the resulting NMR signal. In the spin-warp experiment, the phase encode gradient is varied (rather than the phase encode time) from scan to scan in a stepwise manner. Therefore, the phase of the spins at location *y* are phase-modulated in a predictable linear fashion. The modulation frequency is directly proportional to the spatial location *y*. Fourier transformation along the phase encoding direction converts the time domain and phase modulation into spatial-frequency domain.

The field of view along the phase encode dimension is related to the gradient step size. Therefore, it is convenient to define the parameter pestep, which is equal to the incremental area of the phase encode gradient pulse, defined by the following equation:

$$\mathtt{pestep} = \int_{t4}^{t7} gpe \cdot dt \qquad \text{[Eq. 16]}$$

The number of 2D phase encode steps to be acquired is determined by the parameter nv. nv experiments are run when the phase encode gradients are set to the values, defined by the following equation:

$$\mathtt{pestep} \cdot (n - (nv + 1) / 2) \qquad \text{[Eq. 17]}$$

In Equation 17, n = 1, 2, 3,... nv. Equation 17 ensures an equal number of positive and negative phase encode gradients are applied during the phase encode time tpe. For example, if nv = 4, the gradient amplitudes are stepped in half-integral units of –1.5, –0.5, +0.5, +1.5

The phase-modulated nature of the imaging experiment would normally produce unwanted dispersion components in the final image. This problem is avoided by phase encoding with both positive and negative values of the gradient to create a pseudo-echo signal along the phase encode dimension that is transformed with pure absorption components. Therefore, as in the case of the gradient echo signal, an absolute value calculation yields an image without the need for any phase correction.

The field of view along the phase dimension is related to the step size of the phase encode gradient and is defined by the following equation:

$$lpe = 1 / (\gamma' \cdot \mathtt{pestep}) \qquad \text{[Eq. 18]}$$

In Equation 18, lpe is the field of view along the phase encode dimension, in cm.

It is important to choose the parameters so that the field of view, lpe, is greater than the spatial frequency spread along the phase encode dimension, or else the spatial components that lie outside the field of view will cause fold-over artifacts.

2.6 Image Resolution

Image resolution defines the ability to separate the signal arising from adjacent regions in the object being imaged. Decreasing the resolution improves the appearance of the actual shapes of the separate parts of an object. An image is displayed as a 2D digitized picture and each digital element is referred to as a *pixel* (or picture element). In the case of a 3D image, each digital element is referred to as a *voxel* (or volume element).

Resolution of an image depends on two factors:

- Frequency spread over the field of view, which is determined by gradient strengths gpe and gro.
- Pixel size, which is determined by the number of complex data points in the readout dimension, np/2, and the number of phase encode steps, nv.

Minimum resolution is determined by linewidth, which determines whether the signal from one region can be confined to a single pixel. Linewidth is mainly determined by spin-spin relaxation time and also susceptibility and inhomogeneity at a specific location in the sample.

Resolution along the phase encode dimension is defined in the following equation:

$$Rpe = lpe/nv \qquad \text{[Eq. 19]}$$

Similarly, resolution along the readout dimension is defined by the following equation:

$$Rro = lro/(np/2) \qquad \text{[Eq. 20]}$$

To illustrate image resolution, assume the image is from a sample consisting of three spheres filled with water, as shown in Figure 12.

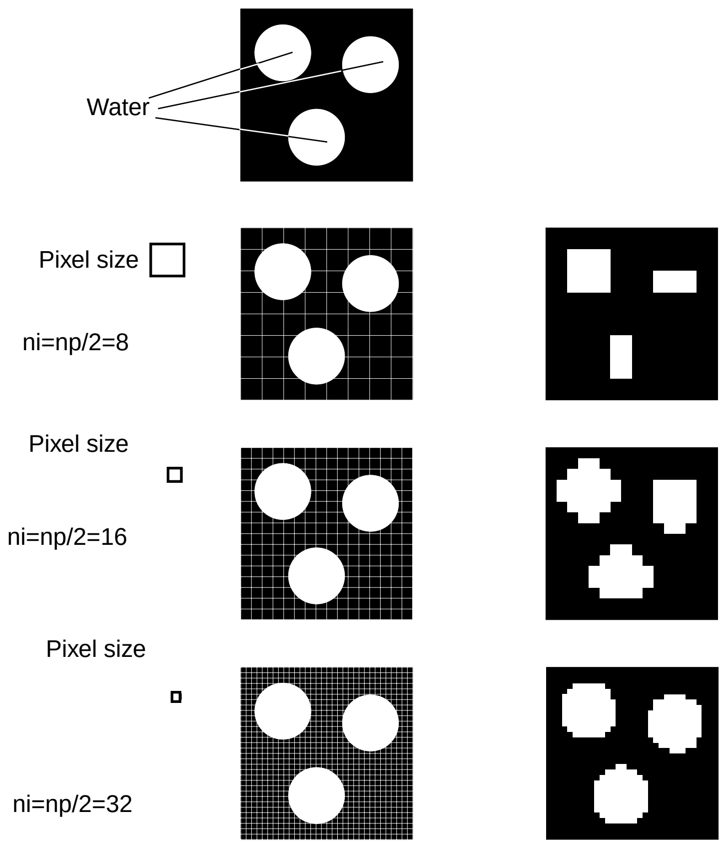


Figure 12. Image Resolution of Three Water-Filled Spheres

When the number of data points is small, one pixel can contain both a large region that does give an NMR signal and a large region that does not give an NMR signal. The lack of NMR signal causes the edges of the object to be poorly defined and can cause overlap between adjacent structures so that the separate objects cannot be distinguished from one another. As the number of data points (and/or gradient frequency spread) is increased, the signal from any given point is better able to be confined to a single pixel, so the amount of overlap between adjacent structures diminishes and the image is better defined.

The usual number of chosen data points is 128 or 256. A smaller number results in insufficient resolution and can also cause artifacts created by truncation of the time domain

signal. A larger number of points along the phase encode dimension (`ni` or `nv`) significantly increases the data acquisition times. More points along the readout dimension increase the acquisition; therefore, the echo times are increased, which leads to loss of signal caused by the T_2* effect. The number of data points is usually set to a power of 2, as required by the Fourier transform. Sometimes image presentation can be improved by *zero-filling*, that is, by increasing the number of image points along the phase and readout dimensions. However, this method does not improve the inherent resolution of the image.

2.7 Spatial Frame of Reference

The section "Image Resolution," page 35, described the NMR method for resolving the spatial dimension along a particular direction. In reality, a sample is a three-dimensional (3D) object. Therefore, it is necessary to be able to resolve the spatial information in 3D space. It is convenient to define a frame of reference for dealing with a 3D sample. The orientation of the magnetic fields produced by the gradient coils inside the magnet defines a coordinate system for imaging experiments. An understanding of the workings of this coordinate system will help you to operate the imaging instrument.

The origin of the whole system lies at the center of the magnet, which is also the center of the gradient coil system. Gradients produce a zero field in the center of the magnet. Therefore, the frequency associated with the origin or magnet center is the resonance frequency for the particular nuclear substance intended for imaging. For example, water is the chemical substance most often imaged for the proton, and the frequency at the origin of the gradient reference frame puts the NMR signal from water "on-resonance."

There are two types of imaging magnets:

- Narrow bore, vertical magnets, which are used for MRI microscopy (MRM)
- Wide-bore, horizontal, magnets, which are used for larger samples

In the case of horizontal magnets, shown in Figure 13, the *z* axis is defined as being in the direction along the bore of the magnet, going from the cable end (back) of the magnet to the sample end (front) of the magnet. The *x* and *y* directions in the horizontal magnets and refer to the left-right and top-bottom orientations respectively, as shown in Figure 13.

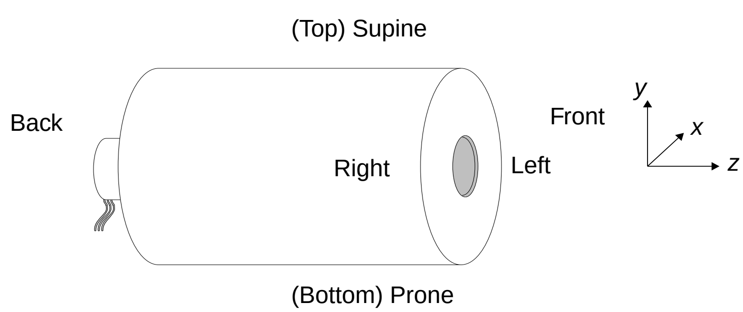


Figure 13. Horizontal Magnet

However the *x* and *y* directions in vertical bore magnets are less obvious because of the cylindrical symmetry of those magnets, shown in Figure 14.

During installation, the gradient coils and shim coils are aligned and fixed so that they are symmetrical with respect to the center of the magnet. For imaging, you must place the rf coil in the magnet center and position the sample within the rf coil.

The image planes are referenced with respect to the gradient frame of reference. The three commonly referenced planes are *sagittal*, *coronal*, and *transverse* and they respectively refer to the planes that are perpendicular to the *x*, *y*, and *z* axes, as shown in Figure 14. Images can also be obtained from arbitrary, or *oblique*, planes. The `plan` macro in VNMR allows you to define oblique planes by using a graphical tool and a reference image. For some applications, you might want to collect a 3D volume image instead of a 2D slice image. For a 3D volume image, it is possible to analyze or view the data by using 3D image analysis routines.

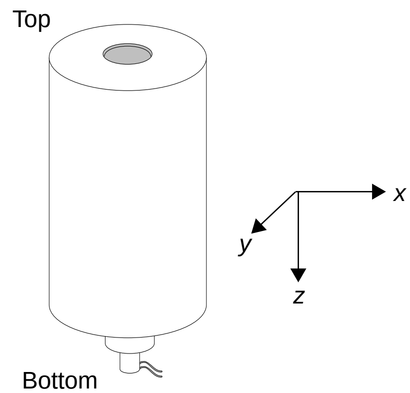


Figure 14. Vertical Magnet

2.8 Image Reconstruction

The imaging data is collected as a 2D arrayed time domain signal, *S(t1, t2),* in which `t1` and `t2` respectively refer to the phase encoding and readout dimensions. (For historic reasons, in conventional 2D NMR, the subscript numerals 1 and 2 respectively refer to the phase encoding and detection dimensions.)

When the signals are viewed along either the phase encode or readout dimension, the time domain signals take the form of an echo signal. Fourier transformation (with respect to `t1` and `t2` using the `ft2d` routine) yields the spatial-frequency data, *S(F1, F2).* The symmetry properties of the echo signal yields only absorption-mode components in the dataset, *S(F1, F2),* without any undesirable dispersion mode components. The yield of only absorption-mode components is a significant advantage in imaging because the final image can be obtained by simply taking the absolute value spectrum, |*S(F1, F2)*|, without the need for any phase correction.

The appearance of the image can be improved or modified by *digital filtering*. Filter functions can either be applied in the time domain or the spatial domain. In the case of time domain data, t=0, point is in the center of the time axis. Therefore, an apodization function symmetrical to t=0 should be applied. For example, a gaussian (“shifted”) function has the effect of improving the SNR of the resulting image at the expense of loss of resolution (“blurring”) of the image. Another common way to improve the image appearance is to *interpolate* the image during the display process. Interpolation is also equivalent to *zero-filling* the data in the time domain.

2.9 Important Imaging Parameters

This section describes three important timing parameters—`tr`, `te`, and `ti`—that are used during the performance of imaging experiments.

tr, Recycle Time

The `tr` parameter defines the time between the beginning of one scan and the next.

It is important to allow sufficient recycling time so that the excited spins have sufficient time to return to equilibrium. In the case of a 90° excitation pulse, a recycle time of >4.T_1 must be allowed. If the recycle time is too short, the signal gets saturated, which results in a gradual loss of signal intensity, eventually reaching an equilibrium or steady-state condition. However, this T_1-dependent signal variation can be exploited to enhance T_1 contrast in the images.

In experiments involving quantitative work such as relaxation studies and pulse power and receiver gain calibration, `tr` must be set to greater than 4.T_1 to avoid erroneous results. In experiments such as FLASH, the flip angle is set to approximately 5° ∞∞to 30° and `tr` is set to small values (about 10 µsec to 50 µsec) so that the images can be acquired very rapidly. Table 2 lists the approximate relaxation times, at 4.7 T, of some commonly used liquids.

Table 2. Relaxation Times

Liquid	*Time*
Doped water (1 g CuS04/liter)	0.6 s
Vegetable oil	0.3 s
Tap water	3 s
Degassed distilled water	26 s

te, Echo Time

Unlike in conventional NMR spectroscopy, imaging experiments usually generate either gradient- or spin-echo signals. The resulting signal intensity therefore depends on the echo time, `te`. Echo time is the time between the center of the rf excitation pulse and the position of the echo maximum, as shown in Figure 15.

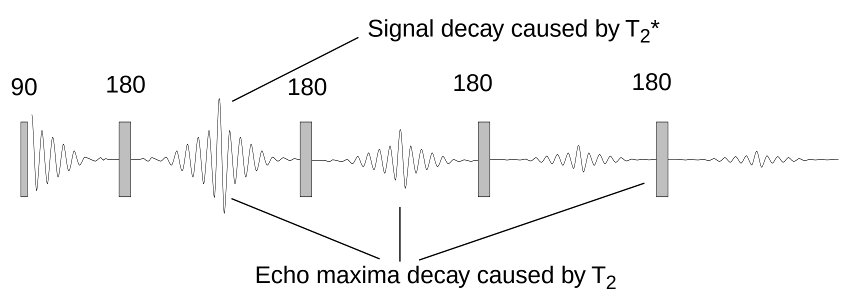


Figure 15. Signal Intensity

Echo time delay results in some loss in signal because of spin dephasing, which is caused by T_2* effects. T_2* is defined as a combination of spin-spin relaxation (T_2), magnetic field inhomogeneity, and susceptibility effects. Susceptibility effects are caused by interactions of the magnetic field with the heterogeneous sample, which produces localized field gradients within the sample. T_2* effects tend to get worse at higher fields. Signal loss caused by T_2* effects is exponential. Therefore, at long `te` values, a dramatic loss of signal intensity can result, leading to degradation of image quality.

It is therefore advantageous and sometimes even necessary to shorten the `te` value to improve image quality. However, there is a limit to the minimum `te` because echo time depends on the acquisition time and the rf and gradient pulse delays in the sequence. The shortest, achievable echo time depends mainly on maximum gradient performances such as maximum gradient strengths, rise times and residual eddy currents. However, `te` delay can also be used to enhance the T_2 or T_2* contrast in images. For example, in functional MRI, brain activity causes localized susceptibility in the brain, which is enhanced by using the

gradient echo imaging techniques. The T_2* effects of solid materials are very short (<100 µs), so special experimental techniques need to be used to obtain images from such samples.

ti, Inversion Time

`ti` is an important contrast parameter in imaging. The inversion time contrast between different components in the sample can be enhanced by performing a `ti` inversion recovery sequence (`ti ir`).

The `ti ir` imaging sequence involves applying a 180° inversion pulse and a delay, `ti`, at the beginning of a conventional imaging sequence. The inversion pulse flips the magnetization to the *z* direction. The spins return to equilibrium, exponentially, with a time constant inversion time, as illustrated in Figure 16.

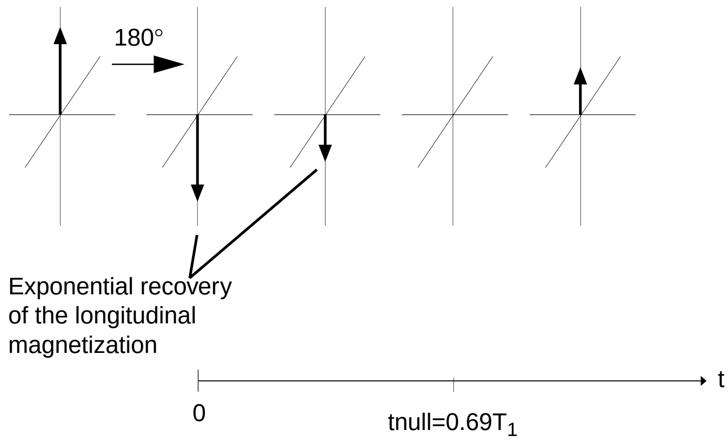


Figure 16. Equilibrium Magnetization

Sampling the magnetization after the inversion time delay results in varying signal intensities, depending on the `ti` of the spins. Notice that the signal is negative at short inversion times and gradually becomes positive at longer inversion times. When `ti=(0.69.T`$_1$`)`, the signal is zero, as shown in Figure 16. If the sign of the intensities is to be retained in the images, it is necessary to phase correct the images instead of taking the absolute value mode. `ti ir` imaging experiments can be inefficient because of the long recycle time required to allow the spins to return to equilibrium.

Chapter 3. Imaging Pulse Sequences

Sections in this chapter:

This chapter describes some pulse sequences for imaging available on Varian NMR spectrometers. You should be familiar with basic operations of the spectrometer; therefore, explanations of operations such as shimming and tuning are not included in this chapter. Refer to the manual *Getting Started* and the VNMR *User Guides* for more information on various spectrometer operations. More detailed descriptions of all commands, macros, and parameters are in the appendix, "Commands, Macros, and Parameters," of this manual and in the manual *VNMR Command and Parameter Reference*.

3.1 Initial Setup

This section describes the procedure for initially setting up imaging experiments using a single-pulse sequence.

The main purpose of the initial setup procedure is to make sure that the system is properly functioning and to determine the rf calibration parameters. Once the initial setup has been completed, the rf calibration parameters, such as transmitter frequency and power, can be used for subsequent imaging experiments and therefore do not need to be repeated. However, if the sample or coil is changed, it might be necessary to repeat the initial setup procedure.

Table 5 on page 62 summarizes the commands, macros, and parameters that are used.

1. Position the sample in the magnet.

   Because imaging coils and samples come in various sizes and shapes, it is important to position the sample and the rf coil in the center of the magnet.

2. Place the sample in the magnet and tune the probe.

   Be aware that different imaging samples can influence the tuning of the probe, depending on their sizes, compositions or even the positioning within the rf probe.

3. Use the single pulse sequence `s2pul` to check for the NMR signal. Initially use a sufficiently wide spectral bandwidth to avoid aliasing of the proton signal.

   The `spuls` macro can be used to load the default parameters suitable for imaging rather than for high resolution spectroscopy.

4. Shim, if necessary.

   Unlike high-resolution spectroscopy, shimming is not critical for most imaging experiments. Even when the linewidths are 50 Hz to a few hundred hertz, good images can be obtained. Typical linewidths for imaging samples such as plant and animal tissues are about 50 Hz to 150 Hz. However, improved field homogeneity can produce better results. Good magnet homogeneity is critical for some experiments, such as echo planar imaging (EPI), gradient echo, multislice imaging (GEMS), and spectroscopic imaging.

5. Use the `s2pul` sequence to set the transmitter frequency on resonance.

   The transmitter offset frequency parameter, `tof`, is needed to define the spatial reference position (the center of the magnet and gradient coils). The macro `setof` automatically determines the spatial reference position using the tallest peak in the spectrum. The offset frequency is then stored in the file `$HOME/vnmrsys/H1offset`. (When running imaging sequences, the macro `ldof` sets the imaging reference frequency parameter, `resto`, to the value saved in the `H1offset` file.) On vertical bore systems, the Z0 shim (B_0 field) can be adjusted so that the transmitter frequency is on the peak of interest (usually water); in which case, `tof` and `resto` parameters are usually set to 0.

   The `offset` macro can be used to determine the frequency offset corresponding to the cursor location. The `movetof` macro can be used to set the transmitter frequency (`tof`) to the cursor position.

6. Calibrate the pulse power. Measure the 90° or 180° pulse and enter it into the `pulsecal` database.

   The `setarray` macro can be used to set up an array of pulse width values for the calibration experiment. The macro `ga` collects and displays the Fourier-transformed data. The command `dssh` allows you to display the arrayed spectra.

   The `findpw` macro lets you more conveniently calibrate the pulse powers. `findpw` automatically determines the maximum and minimum signal from a set of ten, predefined pulse lengths and enters the calibration values into the `pulsecal` database. Once the pulse power is calibrated, pulse parameters such as pulse width (`pw`) and shape (e.g., `pwpat`) in imaging pulse sequences can be easily changed. Pulse powers are automatically computed by the `imprep` routine. Different imaging samples can affect the tuning (Q) of the imaging coil. Therefore, it is necessary to calibrate the pulse with each sample so that the proper pulse powers are calculated for the imaging sequences.

3.2 Conditions for Use

This section lists the conditions that are necessary to use imaging pulse sequences, and information on the `lock` and `spin` parameters and the `spuls` and `s2puls` macros.

Receiver Gain Adjusted

Imaging samples generally produce excessive NMR signals that often saturate the receiver. If the ADC overload error message is displayed, you must set the gain to a lower value. It might also be necessary to further attenuate the incoming signal by manually setting a signal attenuator or by setting the parameter `presig='l'` to `presig='h'`. The macro `setgn` automatically sets the receiver gain, based on the input signal.

Recycle Time Adjusted

When setting gain or measuring pulse power, you must increase the predelay parameter (`d1`) or recycle time parameter (`tr`) to greater than 4*T_1 to allow the spins to return to equilibrium before subsequent rf pulses.

Lock, Spinner, Decoupler Commands and Parameters Disabled

If you use a spectrometer that is also used for high-resolution spectroscopy, make sure that the commands and parameters relevant to the lock, spinner, and decoupler are disabled. The commands and parameters are disabled when they have the following settings:

```
homo='n'
lock='u'
lockpower=0
spin=0
spin='n'
```

The `spuls` macro is convenient for loading `s2pul` pulse sequence parameters for imaging systems. (The `s2pul` macro is used in high-resolution spectroscopy and might incorrectly initialize the parameters for imaging.)

Pulse Power Set Low

Imaging spectrometers are usually equipped with high-power rf amplifiers. Make sure that the pulse power is set sufficiently low to avoid any damage to the rf coil.

Gradient Calibration File Created

Imaging systems can be equipped with either a single gradient coil or multiple gradient coils. The gradient calibration information, or file, corresponding to each coil must exist in the `/vnmr/imaging/gradtables` directory. Use the `creategtable` macro to create the gradient calibration file.

Gradient Amplifier On

The gradient amplifier must be turned on and enabled before proceeding with the initial setup procedure. Be aware that *x*, *y*, and *z* shimming is done via the gradient coils and that the amplifiers can generate a small dc offset current that must be corrected by shimming.

Eddy Current Compensation Files Loaded

If you have a microimaging system with the computer-controlled analog eddy current compensation, use the program ecctool to load the appropriate file. For systems equipped with digital eddy current compensation (DECC), use the decctool program, described in Chapter 8, “Digital Eddy Current Compensation,” to load the appropriate file.

Shim Power Supply Turned On

The shim power supply must be turned on for shimming purposes during experiments. If the shim currents are high, they can generate excessive heat in the bore of the magnet. Air or water cooling is employed to remove the excess heat buildup in the magnet. If the system is not being used for extensive periods or if the air or water cooling is turned off, turn off the shim power supply.

Pulse Calibration Done

Imaging sequences expect the rf calibration information to be present in the `pulsecal` database. The `rfcoil` parameter must be initialized to the entry in the `pulsecal` database.

Air or Water Cooling Turned On

Air or water cooling systems must be enabled for gradient experiments. Cooling is necessary to remove the heat buildup in the bore of the magnet caused by the gradient and shim coils. Gradients systems are usually equipped with protection devices to detect and shut down the amplifier in the absence of either air or water flow.

3.3 GEMS Multislice Imaging

This section describes the steps involved in setting up experiments and collecting imaging data using the gradient recalled echo sequence, which is also known as FLASH™ or GRASS™. Because the setup procedure for most imaging experiments is similar to that of the GEMS sequence, read this section before proceeding to other imaging sequences.

Requirements

Your system must be configured for imaging, and gradient calibration and eddy current compensation procedures must have been completed. Gradient calibration and eddy current compensation are usually done during installation of the system, so you do not need to repeat those procedures. If those procedures have not been done, contact your system administrator.

Description

GEMS is essentially the same as the 2D spin-warp sequence described in "Basic Imaging Principles," page 25. GEMS uses the Fourier transform principle to convert 2D time domain signals to a spatial-frequency domain (image). Most of the other commonly-used imaging sequences can be regarded as variations of this basic sequence. GEMS uses a single excitation pulse; therefore, the pulse flip angle can be reduced at the expense of signal-to-noise ratio. The main advantage of using a smaller flip angle is that the sequence can be rapidly repeated using a shorter repetition time (`tr`). This advantage enables you to obtain images in about one second.

Imaging Sequence

The initial excitation pulse is a slice-selection pulse designed to excite a specific slice in an object. The slice offset is specified by the parameter `pss` (in cm) and its thickness, by the parameter `thk` (in mm). The flip angle of the excitation pulse is usually set to about 5° to 30° so that each scan can be rapidly repeated with a short recycle time (`tr`). Because rapidly repeated scanning is an important feature of the GEMS sequence, it is commonly used in situations in which rapid image acquisition is the primary goal.

For a gradient echo to be generated by the read gradient, the signal must first be dephased and then rephased, as shown in Figure 17. The Fourier transform (`ft`) of the echo signal yields a profile along the readout direction. During the initial setup process, you can view the echo and its profile by setting the number of phase encode steps, `nv`, to 0. The profile

can be used to position the sample (along the readout direction) in the magnet. It can also be used for pulse calibration and for setting the receiver gain.

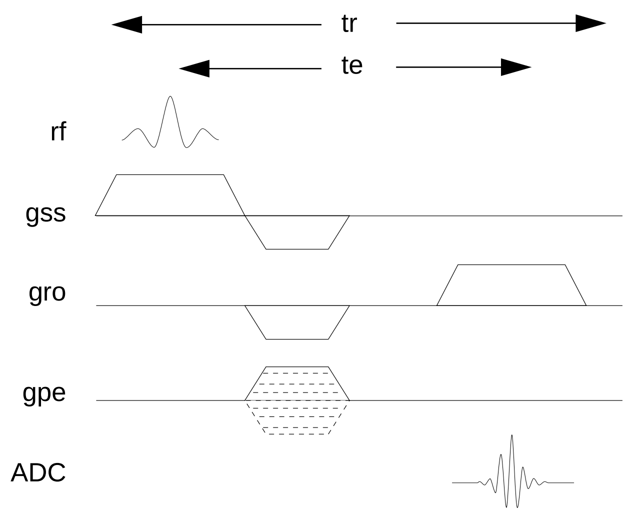


Figure 17. Gradient Echo Imaging Sequence

Data Collection

Set `nv`, the number (64 or 128) of phase encode steps, before entering `go` to acquire the image. For efficiency, the GEMS sequence collects the data in a compressed format (`seqcon='nscnn'`).

If the data is collected in the standard (noncompressed) format (`seqcon='nssnn'`), the overhead in the end-of-scan operation can influence the true recycle time in the pulse sequence. This situation is particularly true for experiments such as GEMS, which is often run with very short `tr` values for recycle time (about 5 msec to 20 msec). In a case when data is collected in the standard format, errors can be significant.

Reformat, Process, and Display

After data collection, use the `flashc` command to convert 2D FID data files from compressed formats (`seqcon='nncsn'`, `seqcon='nccnn'`, `seqcon='nnccn'`) to the standard format (`seqcon='ncsnn'`) or from the standard format to compressed formats.

`flashc` reads the file `fid` in the `acqfil` subdirectory of the current experiment. Because data is reordered and the original `fid` file is overwritten (and therefore *lost*), `flashc` is written so that, in the event of an error during processing, the original `fid` file is preserved. Also, before `flashc` runs, the command does a simple check to prevent it from being executed more than once in an experiment on the same data set. The check looks for the parameter `flash_converted` created by `flashc` when it is run. In order to rerun `flashc`, you must remove the parameter with the following commands:

```
destroy('flash_converted')
destroy('flash_converted','processed')
```

Arrayed or Multislice Compressed Data

In previous versions of VNMR, arrayed or multislice compressed images (`seqcon='nscnn'`) had to be reformatted to a standard 2D format and `flashc` had to be used before the `ft2d` routine could be performed on the data. Now, this method is no longer necessary. By using the command `ft2d('nf',<index>)`, you can improve processing time by reformatting data from the standard format to the compressed format. However, for compressed-compressed 2D data (`seqcon='nccnn'`), you must run `flashc(...)` or `flashc('nf',...)`.

3D Data Sets

`flashc` is not needed for 3D data sets. Use the `ft3d` routine on standard, compressed data (`seqcon='nncsn'`) or compressed-compressed 3D data (`seqcon='nnccn'`).

Compressed-compressed or Standard to Compressed Format

When `ft2d('nf',<index>)` is used, you need to use `flashc` only when converting a compressed-compressed multislice, multiecho, or multi-image sequence. However, for a large standard multislice experiment (`seqcon='ncsnn'`), converting data to a compressed format can be highly beneficial.

Compressed to Standard Format

`flashc` can convert a compressed-compressed multislice, multiecho, or multi-image sequence. It can also convert a “rare” type sequence with a compressed phase-encode echo train.

Processing and Displaying Reformatted Data

After the data has been reformatted, use the `ft2d` command to process and display the 2D image. Instead of using `flashc` and the `ft2d`, the command, use `ft('nf')` to double-Fourier transform the 2D data set. When `ft('nf')` is used, the data is not reformatted. Use the `dconi` command to redisplay the image for further analysis.

Converting Table-Ordered Data

It is possible to acquire data from imaging and 2D experiments in nonmonotonic order, either by explicitly coding the desired progression into a pulse sequence or by using an external AP table to control the order. In either case, VNMR is not able to properly process the resulting data. In such cases, the `tabc` macro is useful.

`tabc` converts data obtained in table order to linear monotonic order so that the data is suitable for processing in VNMR. The data must have been acquired according to a table in the `tablib` directory.

`tabc` reads the file `fid` in the `acqfil` subdirectory of the current experiment. Before data is reordered, this file is written to another file named `fid.orig` in the same `acqfil` directory. Therefore, if for any reason `tabc` fails or results in an unpredictable or undesired transformation, you can salvage the original raw data by moving `fid.orig` back to `fid`. To gain more disk space, explicitly delete `fid.orig` after you are satisfied that conversion is successful.

You can use `tabc` on either saved data that has been loaded into a VNMR experiment or on data in an experiment that has just been acquired but not yet saved. In the first case, you have to save the converted data again if you want the saved data set to reflect the conversion.

`tabc` supports all 2D data types recognized by VNMR: arrayed, compressed multislice, and arrayed compressed multislice.

`tabc` requires that data must have the same number of "traces" as the table elements. It is primitive in what it expects to find in a table file, does not support any of the advanced features of table expansion (e.g., the entire table must be explicitly listed in the table file), and expects to find only one table in a file; whether the table is t1 or t60 is unimportant.

Table Conversion Commands

The following commands apply to table conversion files:

- `tcapply` rearranges the spectra in a 2D data set that resides in the current data file. You must apply `ft1d` to the data before you can use this command.
- `tcopen` explicitly reads, sorts, and stores, in memory, a table conversion file in `$vnmruser/tablib/<file>`, `tcopen` uses the file when `tcapply` is called.
- `tcclose` removes a table conversion file and frees the memory used to store the sorted table indices read in with the `tcopen` command.

Setup Macro

The macro `gems` loads the default parameters from the file `gems.par` into the current experiment. `gems` first searches for a parameter file in your `parlib` directory (`$HOME/vnmrsys/parlib`) and loads the file if it is present; otherwise, the file from the `/vnmr/parlib` directory is chosen.

Because the parameters in the system directory might not always be suitable for your particular application, you should use `svp` to save a parameter file in `parlib` to suit your application needs. If there are multiple parameter files saved in your `parlib` directory, use the `rtp` macro to retrieve the relevant parameters into the current workspace. The macro `rt` retrieves FIDs from a file (`file.fid`) into the current experiment. If `file.fid` does not exist and `file.par` does, `rt` retrieves the parameters from `file.par`.

Advantages

GEMS has a number of advantages, some of which are listed in the following sections.

Fast Imaging

GEMS can be used whenever a quick image is required. It is possible to obtain GEMS images in less than a second. For example, GEMS is commonly used to get a quick image during setup for positioning the sample or for "planning" oblique slices.

Time-Course Studies

Because GEMS images can be obtained in about 500 msec to 1000 msec, it is ideal for time-course studies such as flow studies. However, changes happening in the sample must be slower than the scan time of an image; otherwise, the image will show artifacts.

Contrast Agent Studies

The short recycle time used in GEMS can cause spins with a long T_1 to be selectively saturated while the spins with a shorter T_1 are enhanced. For example, in contrast agent studies, the signals from normal tissues can be suppressed while those containing contrast agents are enhanced.

Angiography

In the case of blood flow studies, stationary spins in the slice plane can be selectively saturated by the rf pulses, whereas spins that are flowing into the imaging plane remain in an equilibrium state and therefore contribute to the signal intensity.

Functional Imaging

Gradient echo sequences (such as GEMS), particularly at high fields, tend to enhance the signal loss caused by susceptibility effects. In functional imaging, brain activation is measured by the susceptibility changes caused by the increased (deoxygenated) blood in the activated regions.

Hardware Requirements

Hardware requirements for GEMS are not as rigid as some of the other fast-scan techniques such as EPI. Therefore, GEMS can be readily implemented on standard imaging systems.

Limitations

The followings sections describe the limitations of GEMS.

Inhomogeneity Effects

During the `te` delay, spins are influenced by T_2, inhomogeneity, and susceptibility effects resulting in the loss of phase coherence (T_2*). Susceptibility gradients are caused by heterogeneous interfaces within the imaging sample. T_2* effects can be minimized by shimming and by reducing the `te` delay. At higher fields, T_2* effects are further enhanced so shimming becomes even more important.

Slice Thickness and Resolution

T_2 * loss and image distortions are caused mainly by phase variations across the slice. T_2 loss can be minimized by reducing the slice thickness.

Similarly, phase variations within a pixel can also cause signal loss. Therefore, increasing the resolution in the image plane (by increasing the matrix size or by decreasing the field of view) can also reduce T_2* loss and distortions. However, reducing the effective voxel size is associated with a loss in SNR. Furthermore, increasing the number of phase-encode steps results in a significant increase in the overall scan time.

Eddy Current Effects

Residual eddy currents act like additional field gradients in the magnet and cause further degradation of the gradient echo signal. Eddy currents can be significantly reduced by using actively shielded gradients or applying gradient “pre-emphasis adjustments” and slew gradient pulses.

Nonsteady-State Artifacts

The brief recycle time used in the GEMS sequence tends to cause a nonsteady-state condition resulting in some residual transverse magnetization. Subsequent rf and gradient pulses can generate stimulated echoes or other spurious signals that can severely distort the resulting images. Gradient and rf spoiler pulses (as discussed by Zur, Y., *Magnetic*

Resonance in Medicine, **21**, 251, 1991) are usually employed in the pulse sequence to minimize such artifacts.

3.4 Obtaining a GEMS Image

WARNING: **GEMS sequences are sometimes run using brief recycle and echo times. Under such conditions, gradient levels can exceed recommended duty cycle or temperature limits. If temperature limits are exceeded, protection circuitry in the gradient amplifiers automatically disables the amplifier. But, some amplifiers do *not* have such protection circuitry. Pay special attention to the duty cycle limits if you are doing imaging on a system without protection circuitry.**

Collecting Non-Time-Course GEMS Images

To obtain a GEMS image, perform the following steps. Table 5 on page 62 lists the commands, macros, and parameters used during this procedure.

1. Initially verify the following conditions before proceeding to the imaging experiment:

   a. The resonance frequency of the signal (usually water) has been determined (and the H1offset file has been initialized with the `setof` macro), as described in the section "Initial Setup."

   b. The rf power levels are calibrated and the entry has been included in the `pulsecal` database.

   c. The appropriate rf amplifier has been turned on and enabled.

   d. The air-cooling or water-cooling accessories are connected and functioning.

   e. The gradient amplifiers are turned on and enabled.

   f. On systems with computer-controlled analog eddy current hardware, the appropriate eddy current file has been loaded by `ecctool`.

   g. The shim power supply has been turned on.

2. Run the `gems` macro to load the default parameters from the `/vnmr/parlib` directory or from your `parlib` directory, `$HOME/vnmrsys/parlib`.

3. Set the parameters for observing the profile.

   `nv` refers to the number of phase encoding values. If `nv=0`, phase encoding is disabled, which allows the profile to be observed. The profile can be very useful for setting up various parameters and for positioning the sample along the read dimension.

4. Set the reference transmitter frequency.

   The resonance frequency of spins corresponds to the position 0 (origin) in the magnet/gradient frame of reference. Therefore, you must set the `resto` parameter equal to the resonance offset frequency. Setting the parameter can also be conveniently done by using the `ldof` macro. (You must have run the `setof` macro to use `ldof`. To run `setof`, see the section "Initial Setup.")

5. Set the rf and gradient calibration parameters.

   The `rfcoil` parameter defines the rf calibration entry in the `pulsecal` database. `rfcoil` allows proper calibration of the rf pulse power in imaging experiments.

Gradient calibration values are saved in a file in the `/vnmr/imaging/gradtables` directory. The `gcoil` parameter must be set to the correct gradient coil entry. On systems with a single gradient coil assembly, `gcoil` is usually set to `'main'`.

If the parameter `gcoil` does not exist in a parameter set and must be created, you must set the protection bit that causes the macro `_gcoil` to be executed when the value for `gcoil` is changed. There are two ways to create `gcoil`:

- Use the macro `updtgcoil`, which will create the `gcoil` parameter if it does not exist and set the protection bits.
- Enter the following commands:

```
create('gcoil','string')
setprotect('gcoil','set',9)
```

6. Set the imaging parameters.

   Check and, if necessary, initialize all imaging parameters. Table 5 on page 62 lists the parameters used in imaging.

7. Prepare the imaging parameters.

   If any of the imaging parameters are altered, the gradient strengths and/or rf amplitude need to be re-evaluated. The `imprep` macro evaluates the new gradient and rf power levels. Execute `imprep` before running an imaging sequence.

8. Optimize the rf power or flip angle.

   `imprep` calculates the rf power level needed to generate a flip angle specified by the `fliplist` parameter (the default is 30). For GEMS, the power is usually set to correspond to about 10° to 30°. To reduce the flip angle by a factor of two, reduce the `tpwr1` value by 6 dB. Using `fliplist` is a more convenient way of setting the pulse flip angle.

9. Check the NMR signal.

   At this stage, all parameters should have been set and should be ready for imaging. Before proceeding any further, check the NMR signal (gradient echo) by typing the command `go`.

   The `df` command displays the FID (echo) on the screen.

   The command `ft` displays the Fourier-transformed signal in the absolute value mode, which is the profile along the readout dimension. If necessary, the sample can be positioned by observing the profile. The gradient echo profile can often appear distorted because of inhomogeneity effects.

10. Optimize the receiver gain.

    To optimize the receiver gain, set `gain='n'` and then execute `go`. After autogain has been adjusted, reset the `gain` parameter (`gain='y'`). To automatically determine receiver gain, use the `setgn` macro. The image profile can be used to optimize the receiver gain.

11. Set the number of phase encoding steps (e.g. `nv=128`).

12. Acquire the image by entering **`go`**.

13. Process the compressed GEMS data by entering the command **`ft('nf')`** or the macro **`ftnf`**. If necessary, use the **`flashc`** command to convert the compressed data to the standard array format.

The `ft2d` command double Fourier-transforms the standard, arrayed, 2D data sets. The `wft2d` command applies apodization functions along the readout and phase encode dimensions before doing a 2D Fourier transform.

14. Display the image by using the `dconi` routine for interactive manipulation. (It might be necessary to rescale the image to the full screen by typing `full` or `fullt`.)

    To adjust the vertical scale of images, move the cursor to a particular part of the image and click the middle mouse button.

You can adjust image brightness and contrast by moving the cursor to the gray scale bar on the right side of the image, and by pressing the left mouse button and dragging the mouse.

Collecting Time-Course GEMS Images

1. For a time-course experiment, set up a list of preacquisition delay values (`pad`). Use the `setarray` macro to set up an array consisting of linear values for `pad`.

   If an exponentially varying delay time is required, use the `exparray` macro.

2. Acquire the data by using the `go` command.
3. Process the data by first using the `flashc` command and then the command `ft2d(index)`, in which `index` refers to the image number.
4. Use the command `dconi` to display and interact with (for example, zoom, adjust brightness) individual images.
5. Use the `dmi` macro to display multiple images.

3.5 Echo Planar Imaging and Phase Correction Map Files

Echo Planar Imaging (EPI) is an elegant technique for very rapidly collecting imaging data in about 25 ms to 100 ms. Using MRI, EPI enables you to monitor changes that occur within fractions of a second. For example, studies that involve motion and flow can benefit from EPI because it not only monitors the dynamic changes, it also minimizes flow-induced and motion-induced artifacts in images. Table 3 shows a list of commands and macros used by EPI routines.

Pulse Sequence

Figure 18 shows the gradient-echo version and Figure 19 shows the spin-echo version of the EPI pulse sequence. The rf pulses are slice-selective pulses very similar to those used in conventional spin-warp sequences (GEMS, SEMS, etc.). The major difference between the EPI sequence and the conventional spin-echo sequence is that in EPI the signal is frequency encoded multiple times by generating a series of gradient echoes. The readout gradient is rapidly switched to generate a train of gradient echoes. The echo amplitudes eventually drop off because of T_2 and T_2* decay.

In the case of the spin-echo EPI sequence, the echo amplitude initially increases because the T_2* effects are refocused at the center of the echo train by the refocusing 180° pulse. Each of the collected echoes is phase encoded by the application of a phase-encoding blipped gradient, as shown in Figure 18 and Figure 19. The main advantage of the EPI sequence is obvious: an entire time-domain imaging dataset is obtained in a single shot.

Table 3. EPI Related Commands and Parameters

Commands	
`dconi`	Displays noninteractive color intensity map.
`epift(index)`	Processes, displays image.
`epiph`	Generates `phasemap` file.
`epirs`	Reverses spectral data.
`epirun`	Collects, processes, displays EPI data.
`episet`	Collects EPI dataset.
`episs`	Load default parameters.
`episvib`	Saves images in Flexible Data Format for ImageBrowser.
`go`	Acquires data.
`pcmapapply`	Applies phase correction map to data (used by `epift`).
`pcmapclose`	Close phase correction map in EPI experiments.
`pcmapgen`	Generates phase correction map (used by `epiph`).
`pcmapopen`	Open phase correction map in EPI experiments.
`ssprep`	Calculates parameters `gss`, `tpwr1`, `tpwr2`.
`svf(file)`	Saves data.
Parameters	
`eff_echo*`	Sets effective echo position in phase dimension (set to `nv`/2)
`gped`	Phase-encode dephasing gradient increment
`groa*`	Readout gradient adjuster in EPI experiment
`grora*`	Readout refocusing gradient adjuster in EPI experiment
`image*`	Phase-encoding gradient flag; 0=off, 1=on
`tep*`	Post-acquisition delay in EPI experiment
* Unique to the `episs.c` sequence	

Data Processing

The echo signals correspond to the 2D k-space data. Note that every alternate echo is acquired with the readout gradient of opposite polarity. Therefore, each alternate echo must be time reversed before it is processed. Time reversal is also equivalent to rotating the corresponding spatial-frequency domain data about the center ($f2=0$).

After the odd echoes have been time reversed, a dataset is similar to the time-domain data collected in the spin-warp imaging sequence. After 2D Fourier transformation, the time domain data yields an EPI image. Figure 20 summarizes the basic data processing steps.

EPI Limitations

Even though EPI is potentially a powerful technique, its has not been widely used because of limitations that include the stringent demands of EPI on gradient hardware and the large gradient fields needed with negligible eddy current effects. Another major limitation is that EPI is prone to artifacts caused by inhomogeneity and the less than ideal nature of field gradients.

In practice, the NMR signal rapidly loses phase coherence because of field inhomogeneity effects and spin-spin relaxation. Therefore, the echo train must be collected in a very short period of time before the signals of interest are lost (dephased). Lost signals can be minimized by shortening the acquisition time. However, if the acquisition time is reduced, the strength of the readout gradient must also be increased by about the same factor.

Consequently, EPI experiments often run into the gradient strength limits. Each blipped gradient phase encodes each echo according to the phase-encode direction. The center of

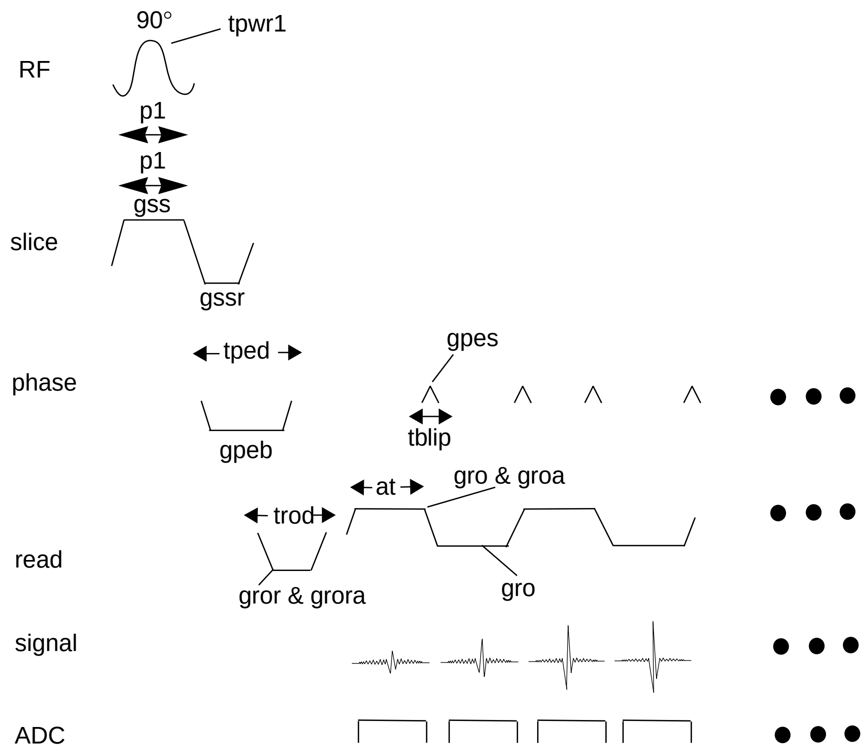


Figure 18. Gradient-Echo Version of EPI Pulse Sequence

k-space along the phase-encode direction is determined by `gped`, the phase-encode dephasing gradient parameter. `gped` is usually set so that the effective echo (`eff_echo`) appears at the center of the phase encode dimension, t1.

Artifacts

Unless special data processing is used, images are usually affected by severe artifacts. Because the EPI is prone to artifacts, the technique is seldom used for routine work. It is useful to know the nature and source of these artifacts in order to understand the steps that are necessary to minimize the artifacts when running EPI experiments.

Half-FOV Ghosts

In an ideal case, all echoes appear at the middle (*t2=0*) of the acquisition window. However, because of the nonideal behavior of gradients and spurious gradient fields, the echo positions of the odd and even echoes might appear shifted from the *t2=0* position, which contributes to the phase shifts between the odd and even echo signals. Half-field-of-view (FOV) ghosts are one of the more common and notorious artifacts in EPI images. These ghosts are caused by incorrect matching of odd and even echoes.

As discussed in "Data Processing," page 52, the evolution of odd and even echoes are time reversed with respect to each other because they are acquired with gradients of opposite polarity. Therefore, external effects (such as inhomogeneity, and eddy currents, etc.) influence the amplitude and phase of odd and even signals in different ways.

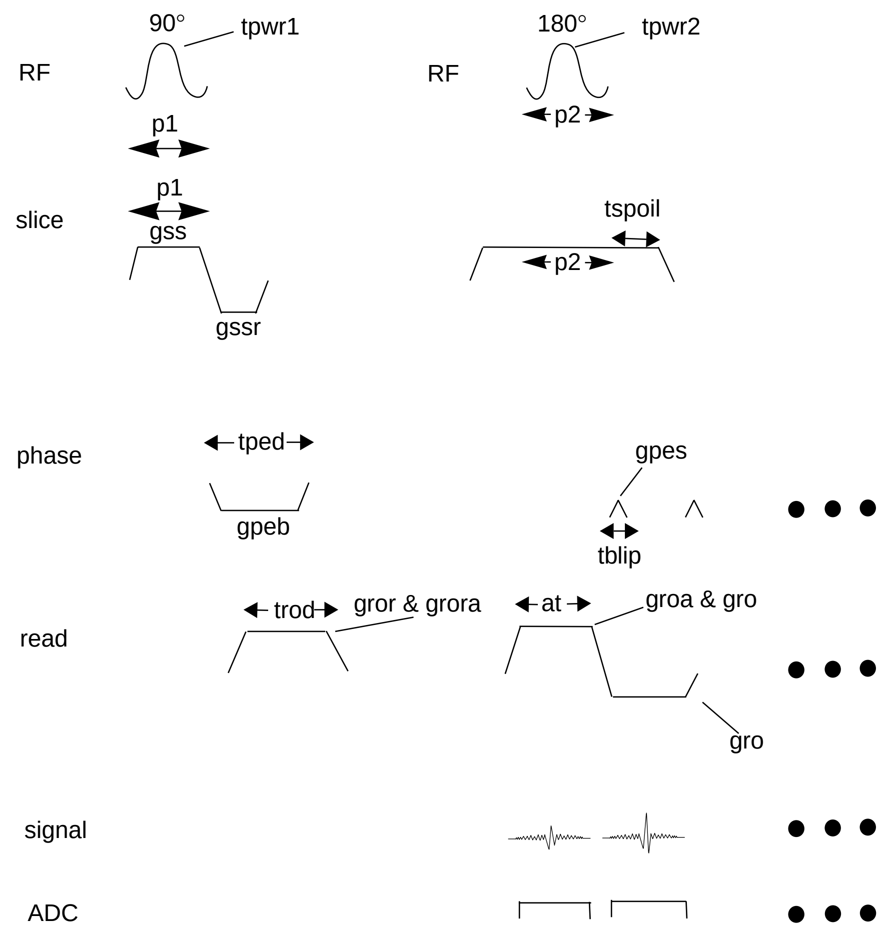


Figure 19. Spin-Echo Variant of the EPI Pulse Sequence

The amplitude and phase variations between odd and even echoes cause a ghost artifact to appear along the phase-encode dimension, as shown in Figure 21. The ghost image appears shifted from the primary image by `lpe/2`; hence, the image is referred to as a half-FOV ghost. Most half-FOV ghosting can be reduced by the EPI phase-correction routines discussed in "Phase Correction," page 57.

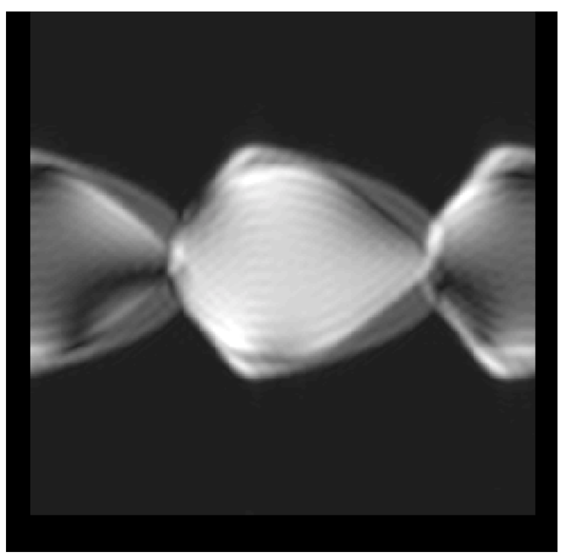


Figure 21. Ghost Artifact

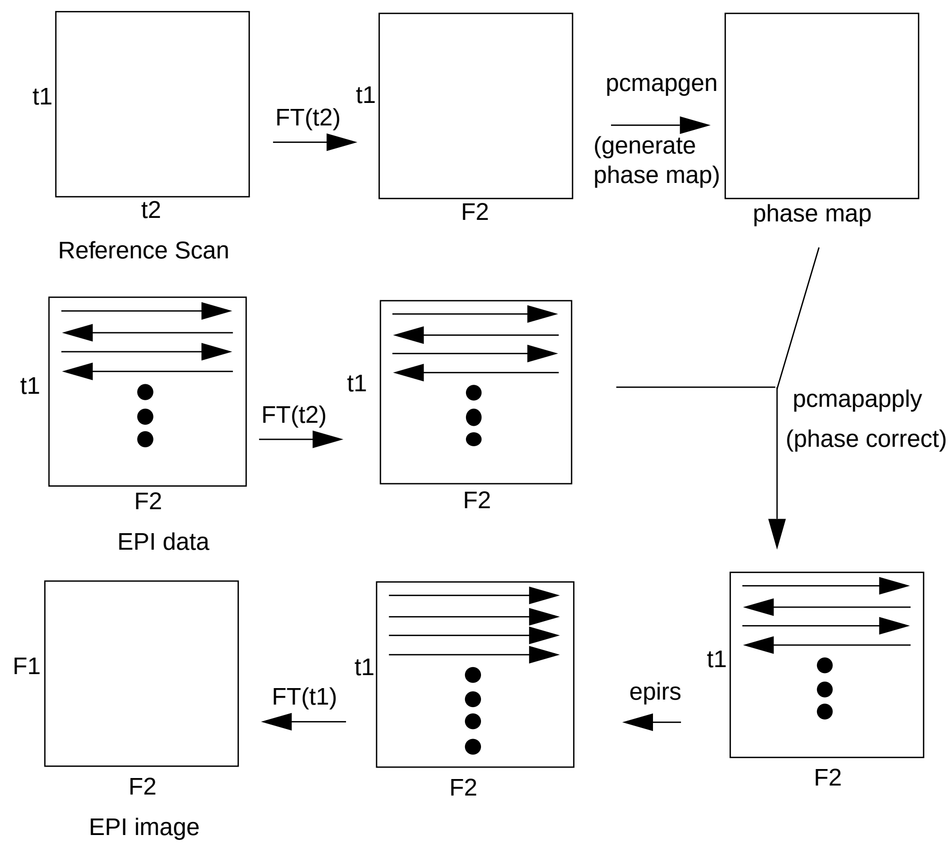


Figure 20. Time Domain Data Processing Steps

Chemical Shift Effects

Unlike the conventional spin-warp sequence, EPI echoes evolve as a function of time. This evolution means that if different chemical components (e.g., oil and water) are present in the sample, each of the echoes in the echo train is also "chemical shift encoded." Therefore, the phase-encode dimension represents both chemical shift and spatial dimensions, which result in multiple images corresponding to the different chemical shift components in the sample. The readout dimension also shows chemical shift artifacts (similar to those seen in conventional spin-warp images), but the effects are much less severe when compared to those seen in the phase-encode dimension. Special pulse techniques are necessary to selectively suppress unwanted resonances. Alternatively, the desired components to be imaged can be selectively excited, which avoids any interference (chemical shift artifacts) from the unwanted resonances.

Phase modulation of the echo signals caused by samples with multiple resonances has another undesirable side effect. Phase modulation caused by the chemical shift effect interferes with the phase correction routines used to correct for the echo shifts along the t2-direction. The `pcmapgen` routine that is used to calculate the phase maps is unable to distinguish the difference between phase shift caused by incorrect alignment of echoes and phase shift caused by chemical shift.

Field Inhomogeneity Effects

Field inhomogeneity effects are caused by either inhomogeneous fields in the main magnet or susceptibility gradients caused by the sample and other materials in the vicinity. Field inhomogeneity effects are also a serious limitation in EPI because they behave like chemical shift effects. These type of effects are also phase encoded and appear as frequency-shifted components in the phase-encode dimension, often leading to severe distortions in the image, as shown in Figure 21. Therefore, shimming is an important part of the EPI setup procedure. (Shimming on the slice should give better results than the usual single-pulse method. A sequence such as `csi2d` can be used for shimming on the slice. When `csi2d` is used, the echo or FID is detected after selectively exciting the slice region.)

Phase Correction Map Files

Homogeneity at the edges of an rf coil is often poor, which can lead to shimming related artifacts in EPI images. Distortions caused in the edges of a sample also affect the phase correction routines used in EPI data processing. Phase correction information is located in the file `phasemap` in the current experiment directory. The commands `pcmapapply`, `pcmapclose`, `pcmapgen`, and `pcmapopen` are useful for working on phase correction map files.

Spurious Gradient Fields

Gradient echo imaging experiments are also sensitive to spurious gradient fields. Therefore, the FLASH sequence can be used as a convenient means of evaluating the progress in shimming. A more elegant approach to shimming is the use of image-based shimming, where an arbitrary region of interest is selected and the shim currents optimized using an analytical method.

Other EPI Limitations

Signal Loss

The data acquisition time (per echo train) for EPI experiments usually lasts for about 25 ms to 100 ms, which is significantly longer than for conventional imaging sequences. Because of the longer acquisition time, the images are heavily T_2* weighted (T_2* refers to the loss of phase coherence of the spins caused by spin-spin relaxation, T_2, and inhomogeneous fields). T_2* weighting can result in a significant loss of signal. However, T_2* weighting can be used to enhance the T_2* contrast in images.

High Gradient Strength

Large gradients are needed for EPI experiments. Therefore, the gradient hardware (gradient coil and gradient amplifiers) must be able to deliver the high gradient strengths required for EPI.

Gradient Switching

The typical acquisition time per echo is approximately 500 µs. Therefore, the rise and fall time of the readout gradients must be sufficiently short so that rapidly switched gradient fields can be generated.

Temperature Increase

In EPI, large gradients are used for relatively long periods of time, particularly during time-course experiments. The gradient hardware must be capable of handling the higher duty cycle that is commonly encountered in EPI. Water and air cooling are typically used to remove the excess heat generated by the gradient coils. The hardware is typically equipped with protection devices to detect unusual temperature increase and shut down the amplifiers. Special precautions are necessary to avoid exceeding the duty cycle limits recommended for a given gradient set.

Eddy Current Effects

Eddy currents create undesirable fields in the magnet region. These fields cause severe artifacts in images. Actively shielded gradients along with eddy current compensation (preemphasis) hardware can be used to minimize eddy currents effects. Slewing the gradients (increasing `trise`) can also minimize eddy currents, but the acquisition times are increased accordingly.

In EPI on vertical bore, high-field microimaging systems, the high spatial resolution and small field of view requirement for microscopy requires very high gradient strengths of the order of 25 to 100 gauss/cm. Fortunately, the smaller diameter gradient coils used in microscopy are also more efficient. Therefore, the high gradient strengths and shorter rise/fall times needed for magnetic resonance microscopy are easily achieved. Note, however, that the residual eddy current fields can also be quite high because of the relatively high gradient strengths used in microscopy experiments. For that reason, actively shielded gradients and additional eddy current compensation hardware are essential to minimize the residual eddy current fields.

Operating at high fields also has its disadvantages; spurious gradient fields (inhomogeneity), susceptibility, and eddy current related effects are enhanced at high field strengths, which make experiments such as EPI more difficult. Any spurious field gradients tend to distort the EPI k-space data in unpredictable ways as shown in Figure 21, resulting in severely distorted images. Therefore, shimming and eddy current compensation often become the more dominant factors in getting good EPI images. Conventional FID shimming using a single pulse sequence often leads to misleading results because the FID is an integrated signal from the whole sample within the rf coil.

For example, if the signal from outside the slice region contains large susceptibility or inhomogeneity field gradients, the shim current values are biased by those regions. Therefore, the imaging slice region might not be optimally shimmed. To obtain the best results, slice shimming is recommended. The region corresponding to the imaging slice is selectively excited and the resulting FID is optimized in the usual way.

Low Resolution

Because of gradient strength and acquisition time limitations, the matrix size for single-shot EPI is limited to about 64×64 or 128×128, which means that EPI images are usually low resolution. Higher resolution images can be obtained by doing multiple scans and then “interleaving” the imaging data, as described on page 58.

Phase Correction

One of the source of artifacts in EPI images is caused by a shift of the echo position in the t2 dimension. The phase shift caused by the echo shift can be corrected by EPI phase correction routines. The phase shift or phase error is determined by collecting a reference scan with the phase encode gradient turned off, using the `episet` macro.

The phase correction procedure is strongly dependent on the quality of the reference scan. For example, poor signal-to-noise ratio of the reference scan data can cause errors in the phase correction calculations. These errors can result in artifacts in the final images.

Advantages

EPI has recently gained in popularity because of the growing interest in functional MRI. Due to advances in gradient technology (namely, actively shielded gradients and special post-processing methods), EPI experiments have become routine in some applications. Collecting images using EPI offers the following advantages:

- Fast images can be obtained in 25 ms to 100 ms.
- Images are T_2* weighted.
- EPI is ideal for studies such as functional MRI, flow studies, and bolus tracking.
- EPI is less affected by motion and flow-induced artifacts.
- The efficiency of other imaging techniques such as inversion recovery (T1) and diffusion, flow can be significantly improved by modifying the basic EPI sequence.
- Pseudo-real time images can be continuously obtained, which makes EPI ideal for time-course studies.

Variations of the EPI Sequence

This section describes four variations of the EPI sequence:

1. Gradient-Echo or Spin-Echo Sequence

The EPI sequence can be either gradient-echo based or spin-echo based. In a spin-echo sequence, inhomogeneity effects are minimized because of the refocusing 180° pulse. However, scan time is slightly increased by approximately 50% multiplied by the echo train duration.

2. Time-Course EPI Experiments

Time-course experiments can be set up by arraying the parameter `pad`.

3. Interleaved Sequences

The limitations of gradient strengths, resolution, and long acquisition times can be overcome by implementing interleaved EPI sequences. In such an experiment, multiple EPI echo trains are collected. Each of the echoes represents segments of k-space data. They are then combined to generate the complete k-space dataset during the post processing stage. However, this type of experiment is no longer a single-shot method. The total scan time for interleaved EPI sequences is increased by TR**n*, in which *n* refers to the number of interleaved experiments.

4. Waveform Shapes

Readout gradients do not need to be rectangular or constant pulses as shown in Figure 18 and Figure 19. For example, the pulses can be trapezoidal or sinusoidal waveforms. There are two advantages of such pulses:

- They are less demanding on the gradient hardware because of the reduced slew rate.

- Eddy current effects are minimized. Eddy current effects are a function of the rate of change of the gradient fields. Note that the gradient fields vary during the acquisition period.

If the collected data is not rectangular, it must be corrected either by post-processing or by nonlinear sampling, so that the final k-space data is regenerated onto a rectangular grid before further image processing. The usual data processing algorithms, such as `ft`, expect the data to collected in a linear fashion.

Experimental Procedure

The following steps perform an EPI experiment.

1. Enter the **`episs`** macro to load the default parameters for single-shot EPI from the default parameter directory.
2. Initialize the imaging parameters. The common parameters are listed in Table 4.

Table 4. Imaging Parameters

Parameters	
`at`	Acquisition time per echo
`gcoil`	Gradient calibration file
`ir`	Inversion recovery flag:0=off, 1=on
`lpe`	Length in phase encode direction (cm)
`lro`	Length in readout direction (cm)
`np`	Number of points in read dimension (real and imaginary)
`nv`	Number of phase encode values
`orient`	Image orientation
`pro`	Position offset in readout dimension (cm)
`pss`	Slice position offset (cm)
`resto`	NMR reference frequency (Hz), set to resonance frequency offset
`rfcoil`	RF coil calibration entry in `pulsecal` database
`spinecho`	1=spin-echo, 0=gradient echo method
`sw`	Spectral bandwidth (Hz)
`thk`	Slice thickness (mm)
`tr`	Recycle time (sec)
`tspoil`	Crusher or spoiler gradient time (sec)

3. Enter **`ssprep`** to calculate the slice-selection parameters.

   Slice gradient (`gss`) and pulse power levels (`tpwr1`, `tpwr2`) are calculated by `ssprep`. You must enter **`ssprep`** whenever slice selection parameters such as pulse width, pulse shape, or slice thickness are modified.

   `ssprep` is very similar to the `imprep` macro, except that `ssprep` does not calculate readout and phase encode gradient parameters. Readout gradients and phase encode gradients are explicitly calculated within the pulse sequence. `ssprep`, unlike `imprep`, allows you to manually set the `at` and `sw` parameters.

   Do NOT use `imprep` *when running the* `episs` *sequence.*

4. Align echoes and generate the phase map from the reference scan.

   a. The echo maxima in EPI ideally should appear at *t2=0*. However, because of nonideal conditions, the echoes appear shifted from this position. To view the echo train and adjust some parameters to shift the echo position towards

t2=0, use the `episet` macro. `episet` optimizes parameters for EPI, collects a reference scan, and allows you to adjust the gradient parameters `groa` and `grora` and the timing parameter `tep`. `tep` controls acquisition delay time, in µs, to allow for propagation of the gradient pulse.

b. Collect a dataset (reference scan) with the phase-encode gradient turned off (`image=0`) and display the echo signals on the screen by using `episet` or by entering the following commands:

`image=0 go df2d`

The echoes might appear tilted. Usually the odd and even echoes appear to line up differently, as shown in Figure 22.

c. Change the tilt by adjusting the `groa` parameter (in ± 0.01 unit steps). At this stage, you might see two parallel echo trains corresponding to the odd and even echoes respectively, as shown in Figure 23.

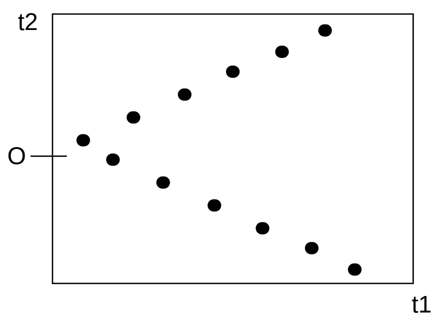


Figure 22. EPI Echo Train

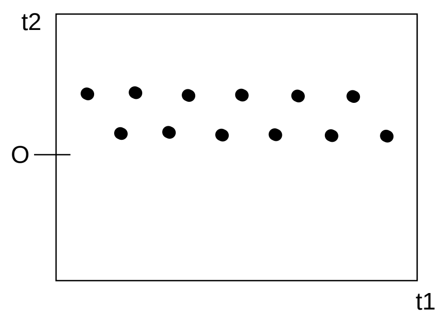


Figure 23. Echo Train After groa Adjustment

d. Adjust the `grora` parameter (in ± 0.1 unit steps) until the echoes line up, as shown in Figure 24.

e. If the echo train is offset with respect to *t2=0*, adjust the `tep` parameter so that the echoes are centered according to t2, as shown in Figure 25. (Note that `tep` corresponds to a delay in µs. Usually, `tep` is set to about 0 µs to 50 µs.)

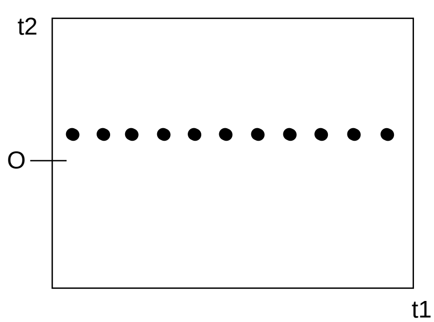


Figure 24. Aligned Echoes

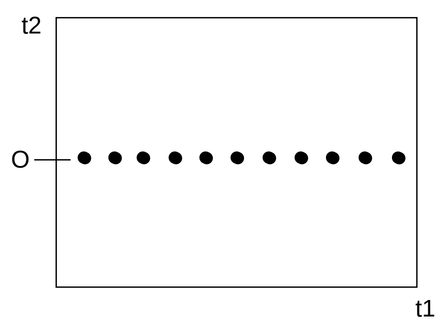


Figure 25. Centered Echoes

f. Use `episet` to generate the phase correction map file (`phasemap`) in the current experiment directory and display the 2D time-domain data. `episet` is equivalent to executing the following commands:

```
image=0 go epiph df2d
```

`epiph` creates the `phasemap` file in the current experiment directory from the reference scan. The first data array must correspond to the reference scan, which is collected with the phase-encode gradient turned off, `image=0`.

5. Acquire and display an EPI image.

   a. Enter the **`epirun`** macro. `epirun` collects, calculates, and displays the EPI image. `epirun` is used to obtain a single EPI image. `epirun` is equivalent to executing the following commands:

      `go epift`

      `epift` processes and displays EPI data in array number, `index`; it is used for EPI processing. The first data array must contain the reference scan. `epift` uses the command `epirs`, which reverses spectral data.

   b. To display the image, use the **`dconi`** command.

Other Ways to Collect, Store, and Process EPI Data

EPI data processing requires a reference scan for calculating the phase map. So, you should collect and store the reference scan as part of the EPI dataset for later processing. The following methods are other ways for collecting, storing, and processing EPI data.

Collecting Images

You can use the `image` parameter to specify single or multiple images.

1. To collect images, set `image` to either of the following values:

`image=0,1`	One EPI image is obtained.
`image=0,1,1,1,1`	Four images are obtained as in a time-course experiment.

   `image=0` refers to the reference scan data. 0=phase encoding off, 1=phase encoding on.

2. Do the following procedure to store the reference scan as the first dataset so that it can be used for subsequent data analysis. The reference scan is used to generate the `phasemap` file, which is used to phase correct EPI datasets.

   a. Enter **`go`** to acquire the data.

   b. Enter **`svf(file)`** to save the data, where `file` is the name of the file to be to save the data.

   c. Enter **`epiph`** to generate the `phasemap` file from the reference scan.

   d. Enter **`epift(index)`** to process and display the image in array number `index`.

Displaying and Manipulating Images

You can display and interactively manipulate the image by using `dconi`.

Viewing Images

You can view the data with the ImageBrowser. To run ImageBrowser, enter **`browser`** on a UNIX command line. Before you can view image data, first convert the data with the **`episvib`** macro. `episvib` expects the first image to be the reference scan.

Zero-Frequency Spike

EPI data is usually collected using `nt=1`. Therefore, any imbalance (dc offset) between the real and imaginary (quadrature) signals, after Fourier transformation, generates a zero-frequency spike in the resulting image. To remove this artifact, enter **`dcrmv='y'`**.

If `nt` is set to a multiple of 2, the phase cycling schemes in the pulse sequence eliminate the artifact. In this case, enter **`dcrmv='n'`**.

3.6 Commands, Macros, and Parameters

Table 5 contains information about the commands, macros, and parameters that are used with imaging pulse sequences. The appendix, "Commands, Macros, and Parameters," contains more information about each item.

Table 5. Imaging Pulse Sequence Commands, Macros, and Parameters

Command	*Function*
`dconi`	Interactively adjusts 2D data displays.
`dssh`	Displays an arrayed set of spectra, stacked horizontally.
`flashc`	Converts compressed GEMS data set into standard VNMR file format. Needs to be executed only once on a data set.
`ft`	Fourier transforms 1D data.
`ft2d`	Fourier transforms 2D data.
Macro	*Function*
`dmi`	Displays multiple images.
`decctool`	Opens tool to set eddy current, slew rate, and related parameters, using digital eddy current compensation (DECC).
`ecctool`	Opens tool to set eddy current, slew rate, and duty cycle using computer-controlled analog eddy current compensation hardware.
`exparray`	Arrays a numeric parameter.
`findpw`	Measures 180° pulse length and updates `pulsecal` database.
`ftnf`	Processes compressed data. It is equivalent to the command `ft('nf')` and can be used for processing compressed data.
`ga`	Acquires and Fourier transforms data.
`gems`	Loads default parameters.
`go`	Submits experiment to acquisition.
`imprep`	Sets up rf pulses, imaging, and voxel selection gradients.
`ldof`	Sets `resto` equal to transmitter offset frequency determined by `setof`. The value of `resto` is changed accordingly. Offset frequency is saved in the global frequency file `$HOME/vnmrsys/H1offset` by the `setof` macro.
`movetof`	Sets `tof` parameter to that specified by cursor.
`offset`	Sets frequency offset corresponding to cursor location.
`plan`	Defines slice parameters using a reference image.
`pulsecal`	Loads rf pulse power calibration parameters.
`rt`	Retrieves FIDs from `filename.fid` directory.
`rtp`	Retrieves parameters from `filename.par` directory.
`s2pul`	Loads default single pulse sequence parameters.
`setarray`	Sets an array of values for a given parameter.

Table 5. Imaging Pulse Sequence Commands, Macros, and Parameters (continued)

`setgn`	Sets receiver gain.
`setof`	Sets spatial reference position.
`spuls`	Loads default single pulse sequence parameters relevant for imaging.
`svf`	Saves current parameters and FID data in `filename.fid` directory.
`svp`	Saves current parameters in `filename.par` directory.
Parameter	*Function*
`d1`	Sets first delay length in standard two-pulse sequence and other pulse sequences.
`fliplist`	Contains a list of pulse flip angles, in degrees.
`fn`	Selects Fourier number in read dimension.
`fn1`	Selects Fourier number in phase dimension.
`gcoil`	Specifies physical gradient set currently installed, and allows updating of gradient characteristics. `gcoil` is a database file containing gradient calibration values from the `/vnmr/imaging/gradtables` directory.
`homo`	Enables homodecoupling control for first decoupler.
`lpe`	Specifies length (field of view) in cm along phase dimension.
`lro`	Specifies length (field of view) in cm along readout dimension.
`np`	Sets number of points (real and imaginary) in readout dimension.
`nt`	Sets number of averages.
`nv`	Sets number of phase encoding steps. If `nv` is set to zero, a profile along the read dimension is obtained.
`orient`	Defines orientation of imaging plane by setting the three commonly used orientations: (1) sagittal (`'sag'`), perpendicular to X axis; (2) coronal (`'cor'`), perpendicular to Y axis; and (3) transverse (`'trans'`), perpendicular to Z axis It is also possible to set the orientation to an arbitrary (oblique) plane by using the `plan` macro. For a more detailed description of `orient`, see Chapter 9, "Parameters."
`p1`	Calculates length of excitation pulse, in µsec.
`p1pat`	Specifies shape of excitation pulse.
`pcmapapply`	Apply Phase Correction Map to Data (C); used in echo planar imaging.
`pcmapclose`	Close Phase Correction Map (C); used in echo planar imaging.
`pcmapgen`	Generate Phase Correction Map (C); used in echo planar imaging.
`pcmapopen`	Open Phase Correction Map (C); used in echo planar imaging.
`presig`	Selects preamplifier signal level.
`pad`	Specifies a preacquisition delay
`pss`	Specifies slice position in cm. Can be entered manually or via the `plan` macro.
`pw`	Specifies rf pulse width, in µsec.
`resto`	Specifies resonance transmitter offset frequency, in Hz. It must be set so that the transmitter is on the resonance frequency of the imaging component, usually water. `ldof` can be used to set this value from the global value in `H1offset`.
`rfcoil`	Contains rf pulse calibration entry in `pulsecal` database.
`tcapply`	Apply table conversion reformatting to data.
`tcclose`	Close table conversion file.
`tcopen`	Open table conversion file.
`te`	Specifies echo time, in sec. For GEMS, it is usually set to less than 0.01 sec to minimize T_2* effects.
`thk`	Specifies slice thickness, in mm.
`tpwr`	Specifies pulse power output, in dB units. 63 dB is the maximum value.

Table 5. Imaging Pulse Sequence Commands, Macros, and Parameters (continued)

`tpwr1`	Specifies pulse power for the excitation pulse. The `imprep` macro sets the pulse power to the value specified by `fliplist`. For GEMS, set `tpwr1` to correspond to a 10° to 20° flip. If the `tpwr1` value is reduced by 6 dB, the flip angle is reduced by 50%. For example, reduction in the power by 12 dB corresponds to a flip angle of 22.5° (90°/4). `fliplist` provides a easy way to change the flip angle.
`tr`	Specifies recycle time, in sec. It must be set to allow for spins to return to their equilibrium state. For GEMS, it can be reduced to about 0.025 sec to 0.1 sec because of the low flip angle (5° to 30°) used for excitation.

Chapter 4. Image Browser

Sections in this chapter:

Image Browser is a comprehensive image viewing and analysis program that reads data saved in the Flexible Data Format (FDF) or in VNMR phasefiles. The program uses mouse-oriented point-and-click methods, and all processing within Image Browser is performed on the data itself and not on the displayed pixel values.

4.1 Overview

This section explains the system requirements for operating the Image Browser program, the layout of the Image Browser screen, processing and graphics functions used by the program, display controls, and data formats.

System Requirements

Image Browser operates on platforms with the following configuration:

- Sun SPARC workstation
- 8-bit or 24-bit frame-buffer
- OpenWindows, version 3 or higher
- Solaris, version 2.3 or higher

The minimum memory requirement is 12 MB; however, more than 16 MB is recommended to enhance performance.

Screen Layout

Figure 25 shows the overall layout of the Image Browser screen.

Control Panel

The control panel consists of command menus where specific operations can be run. A command might process the data, display an image, or open another window.

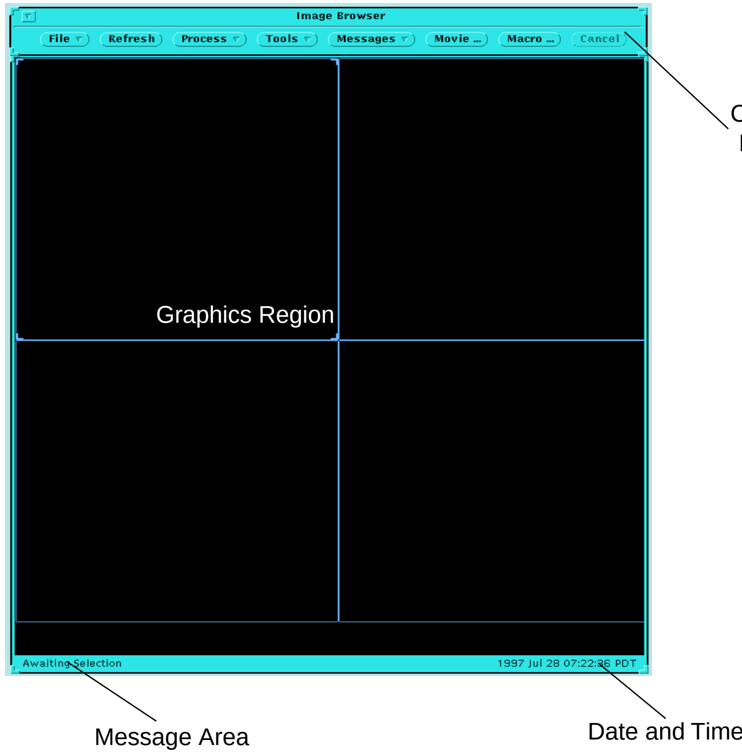


Figure 25. Default Layout of Main Image Browser Screen

Graphics Region

The graphics region occupies the largest portion of the screen. All graphical drawings and images are shown inside the graphics region, which can have a number of graphics frames (Gframes) where images are displayed. Before an image is displayed, a Gframe at a specific location with the desired frame size must be created. An image is automatically resized to fill the Gframe, without losing the aspect ratio of the image. Besides images, regions of interest (ROIs) can be created, lines can be drawn, and text can be placed in the graphics region.

Message Area, Date, and Time

Below the graphics region, informative messages are displayed in the lower-left corner of the window frame. This is the standard way in an Open Look user interface to display messages. Error messages are displayed in a separate window. In the lower-right corner, the date and time are displayed.

Processing Functions

Image Browser provides a number of processing functions:

Statistics	Mean intensity, standard deviation, maximum, minimum, median, area, and volume can be calculated on one ROI or a number of selected ROIs. Statistics are plotted when more than one ROI has been selected. For example, mean intensity might be plotted against the Z coordinate of the slice. An intensity histogram is generated when one ROI has been selected.

Filtering	Images can be processed using a 3×3 or 5×5 pixel convolution filter. Default filters can be selected, or user filters can be generated and saved.
Enhancement of images	Images can be processed using equalization, low-intensity emphasis, high-intensity emphasis, and hyperbolization histogram methods.
Arithmetic functions	Images can be arithmetically combined with other images or constants.
Image rotation	Images can be rotated (in increments of 90°) and reflected.
Line functions	Intensities can be viewed as traces on a line or projections across a line. Distances can be viewed on the line.
Cursor functions	The coordinates and image intensity can be viewed at a cursor location. The distance between two cursors, either in the same image or in different images, can be also be viewed.

Graphics Functions

Tools are provided to create and modify various types of objects in the graphics region. Examples of objects are graphics frames that hold images, ROIs that define regions of the images, cursors that define locations on the images, and text annotation on the images.

Image Browser uses an 8-bit frame buffer, which can show only 256 colors or gray levels at a time. The default colormap structure is 64 levels for grayscale and 12 levels for miscellaneous. On 24-bit graphics machines, about 200 levels of grayscale can be used.

Image Animation

Image Browser provides an option to sequentially display images in a single Gframe. This option allows images to be browsed or an animated image to be produced, similar to a movie.

Macros

Image Browser incorporates the MAGICAL II macro programming language. MAGICAL can greatly speed up work that involves repetitive tasks.

Display Control

Various image display parameters can be manipulated with some of the graphics tools. For example, the vertical scale tool controls the intensity and contrast of the display, and the zooming tool allows part of an image to be seen in more detail.

Data Formats

Image Browser supports two input data types: VNMR phasefile format and Flexible Data Format (FDF). Because of limitations in the phasefile format, using FDF is preferred. A number of data formats are supported for output.

4.2 Getting Started

This section describes the process of verifying the correct user environment, starting Image Browser, and performing some of the basic functions.

User Environment

Image Browser has been designed to run in an X Window System environment. This means that any X terminal can be used as the user interface as long as it supports the 8-bit graphics. However, for Image Browser version 5.3, the host system that runs Image Browser must be a Sun SPARC workstation running Solaris 2.3 or higher. If your X Windows manager does not support the OpenLook interface, some Image Browser features may be unavailable. In particular, some window managers do not support pinup menus.

If a large number of images must be processed at once, the host system should have as much memory and swap space as possible. In particular, smooth image animation displays require that the X display server have enough memory to simultaneously keep all the images in the movie in memory.

For systems with imaging software, the `/vnmr/user_templates/.cshrc` file should contain the following statement:

```
setenv BROWSERDIR $HOME/ib_initdir
```

If a new user is created with the `makeuser` script, this variable is automatically set. `BROWSERDIR` points at a user initialization directory.

Initialization Directory

The initialization directory `ib_initdir` contains the files, bitmaps, frame directories, ROI directories, and filter directories used for starting up, tuning, and running Image Browser. This directory is in `/vnmr/user_templates` and is copied into the user's home directory when `makeuser` is used. This directory can be copied into any location within the user's area as long as the environment variable `BROWSERDIR` is set to point to the new location. All files ending with a `.bm` are bitmap files and should not be changed.

The initialization directory contains the following relevant files and directories that have useful and important information:

`colormap.init` — File containing the colormap definition. Colors for Gframes, ROIs, and text annotations can be personally defined. The number of grayscale levels can also be reduced if colormap flashing is a problem; levels can also be increased if more intensity resolution is desired. Machines with 24-bit frame buffers should not exhibit flashing problems with Image Browser. For those machines, set the number of gray levels to 200 by changing the `64` to `200` in the line `gray-color 64 DEFAULT_GRAY_COLOR`.

The number of colors available for ROIs and labels can also be increased by changing the `12` in the line “`mark-color 1`” to whatever is desired and adding lines specifying RGB values to the list that follows that line.

`macro` — Directory containing user macros and, in particular, the macro `startup`, which is executed when Image Browser starts. `startup` might load a set of Gframes and set various options, such as the gamma correction settings.

`window.init`	File containing the default positions for the main Image Browser window and various popup windows.
`gframe`	Directory containing the supplied Gframes. The file `default` in `gframe` is the set of Gframes that are loaded at startup. In this directory, or a subdirectory, sets of Gframes can be saved. A personal default set of Gframes can be created by overwriting the current `default` file.
`roi`	Directory, possibly with subdirectories, in which any created ROIs for loading onto a set of images can be saved.
`filter`	Directory containing the supplied convolution filters. Personal filters should be saved here or in a subdirectory.

Starting Image Browser

Image Browser is started by typing the command `browser` on a UNIX command line. The following examples show the command line syntax for `browser`:

```
browser
browser <macro_name>
browser <XView_arguments>
browser <-image path_name>
browser <-imagelist path_name>
```

`browser` arguments can appear in any order.

- `macro_name` is the file name of a macro, which must be stored in `$BROWSERDIR/macro/macro_name`. The macro is executed when Image Browser starts. If no macro name is specified, the macro `startup` is executed.
- `XView_arguments` are any type of standard XView arguments, which can be found by typing `man xview` on a UNIX command line.
- `-image path_name` specifies the full path of an image that should be loaded at startup. It is loaded after the `startup` macro is executed. Multiple `-image` arguments can be used to load multiple images.
- `-imagelist path_name` specifies a file containing a list of file names of images to be loaded.

When Image Browser starts, it reads the file `colormap.init` to initialize the colormap and the file `window.init` to initialize the window locations and sizes on the screen. It also starts two processes: `ib_ui`, which runs the Image Browser control panel, and `ib_graphics`, which controls everything else, including processing and graphics.

Using the Mouse Buttons

Because this is a point-and-click based tool, you need to be familiar with mouse buttons and command panel functions before manipulating frames and loading images. General use of mouse buttons is described in the *OpenWindows User's Guide.* The following information describes how mouse buttons are used in Image Browser.

Left Button: SELECT

In the control panel, use the *left* button to select buttons.

In the graphics region, use the *left* button to choose an object or to draw an ROI or text annotation. Selecting an object deselects any previously selected objects. Objects that can

be selected include graphics frames, images, ROIs, and text annotations.When an ROI type or annotation is selected in the graphics tools panel, the *left* button initiates the drawing of the ROI or placement of new text.

Middle Button: ADJUST

The *middle* button is not used in the control panel.

In the graphics region, use the *middle* button to toggle the state of an object, select it if it is not selected, and deselect it if it is.

Right Button: MENU

In the control panel, use the *right* button to display menus.

Using the Control Panel Menus

The control panel, shown in Figure 26, contains a set of basic command options.

Figure 26. Image Browser Control Panel

Buttons with an arrow (▽) have submenus that are activated by the *right* mouse button. The *left* button can also be used to select the default choice. The action of submenus processes data, opens a window, etc., depending on the functional operation. A button with three dots following an item's name (e.g., Macro...) opens a popup window rather than immediately performing the selected action.

The Cancel button, at the right end of the control panel is normally “faded” and cannot be selected. However, performing a potentially lengthy operation, such as loading all the images from a directory, activates the Cancel button. Selecting the activated Cancel button aborts the current operation.

See “Graphics Tools,” page 80, for more information about the control panel menu option Tools.

Creating and Manipulating Graphics Frames

The Frame button must be selected when performing any of the Gframe functions other than selecting a Gframe.

To select the Frame button:

1. Position the mouse pointer on the Tools button in the control panel and press the *left* mouse button. The Tools popup window opens.
2. Select the Frame button  to activate the Frame tool and display Frame Properties in the Tools menu.

3. Position the pointer over the Frame Properties button and hold down the *right* mouse button until the menu shown in Figure 27 appears.

   You can now work with Gframes.

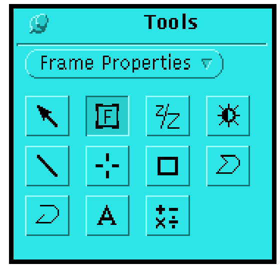


Figure 27. Frame Properties Menu

To select a Frame Properties command:

1. Hold down the *right* mouse button and move the cursor down the list of commands.
2. When the desired command is highlighted, release the button.
3. “Pin” the menu by selecting the pushpin icon  in the top left-hand corner of the menu.

Creating Gframes

To create new graphics frames:

1. Position the mouse pointer in the graphics window (outside of any existing Gframe).
2. Hold the *left* mouse button down and drag the pointer across the screen. This action draws a box.
3. When the *left* button is released, the box is completed and selected. Notice that a frame must not overlap any part of another frame.

Another way to create a Gframe is to load an image when no frames exist. A Gframe the size of the whole graphics region is created, and an image is loaded into it.

An array of Gframes can be created from an empty graphics region with the Gframe splitting routine described in “Splitting Gframes,” page 72. If no Gframes exist, the entire graphics region is split up into the requested matrix of frames.

Selecting Gframes

To select a graphics frame:

- Position the pointer within the frame and click the *left* button.

  The frame’s corners become highlighted to show that it is selected and any other selected frames are deselected.

To select a number of frames:

- Press the *middle* mouse button to select a frame if it is not selected, or deselect it if it is already selected.

To select a number of Gframes and append each frame to a selection list:

- Enable the Frame tool and select each frame with the *middle* mouse button.

  There is also a selection in the Frame Properties menu that selects all Gframes. Gframes can also be selected when the ROI Tools button (designated by an arrow) is enabled in the Tools popup window.

Moving Gframes

To move a Gframe:

1. Select the frame.
2. Position the cursor within the selected Gframe, and hold down the *left* mouse button.

3. Drag the frame to a new location.

   Gframes can be dragged across other Gframes, but must not be dropped where they would overlap with another Gframe.

Resizing Gframes

To resize a Gframe:

1. Select the frame.
2. Position the cursor on the desired highlighted corner, and hold down the *left* mouse button.
3. Drag the corner to the desired position.

Splitting Gframes

Splitting Gframes into a number of smaller frames allows viewing formats to be quickly and easily set up. To split a Gframe:

1. Enable the Frame tool.
2. Select the Gframe or frames to be split.
3. Choose the desired split from the Split Selected Frames menu in Frame Properties.

Saving Currently Displayed Gframes

To save all currently displayed Gframes:

- Select the Save Frame Layout option. It switches the File Browser to Graphics Frame Save mode. Use the File Browser to go to the desired directory and save the frames.

Storing and Retrieving Gframes

Gframe files are stored into and retrieved from the directory `$BROWSERDIR/gframe` or a subdirectory of `gframe`. Gframes are retrieved with the same size and positions with which they were stored. They are not adjusted to fit the size of the graphics window. If any of frames are entirely outside the current graphics region or overlap with existing frames, those frames are not loaded.

To store Gframes:

- Select the Save menu in the Frame Properties menu.

To retrieve Gframes:

- Select the Load menu in the Frame Properties menu.

Deleting Gframes

To delete graphics frames on the screen:

- Select the Delete option in the Frame Properties menu to delete all the frames on the screen. You can also delete all of the “selected” frames, all the “unselected” frames, or all the frames without images.

Clearing Gframes

To clear images out of the Gframes:

- Select the Clear command in the Frame Properties menu. The Clear command has several options: it clears all frames, clears selected frames, or clears unselected frames.

Using File Browser

Many functions that read or write user-selected files use the File Browser tool. The initial File Browser directory is the directory in which Image Browser started.

Changing Directories

To change directories, do one of the following actions:

- Double-click on a directory selection.
- Click on a selection to put the directory name onto the top line and then press the Return key.
- Enter a full directory name, followed by a Return. You can use the ~ identifier in the same manner as in the C shell to represent your home directory.

Saving Images from VNMR for Image Browser

Images can be saved from VNMR by joining an experiment in VNMR with image data, and then running a macro that saves an image or multiple images to disk.

For current imaging pulse sequences (SEMS, MEMS, SEDIFF, FLASH, etc.), the macro is `svib(directory)`. For example, entering **`svib('mydata')`** on the VNMR command line creates the directory, `mydata.dat` in the current VNMR directory. One or more images can then be saved in `mydata.dat`. Images are named `image0001.fdf`, `image0002.fdf`, `image0003.fdf`, etc.

For older SIS imaging pulse sequences and microimaging pulse sequences (IMAGE, SHORTE, SSFP, etc.), the macro for saving images is `svsis(directory)`. Thus, entering **`svsis('mydata')`** on the VNMR command line creates the `mydata.dat` directory in the current VNMR directory. Images can then be saved in `mydata.data` as `image0001.fdf`, `image0002.fdf`, `image0003.fdf`, etc. If `svsis` does not know about the pulse sequence, edit the macro to define the sequence name and type.

3D image data sets can be transformed and saved in FDF format with the `ft3d` macro.

If no image data is available on the system, a file named `image.4T.fid` in the directory `/vnmr/fidlib` can be retrieved. You can then save an image by entering the command **`svib('image.4T'`**`)`.

Loading Images

Images are easily loaded in Image Browser. Select the File button, which opens a File Browser Data window. You can now browse directories and data files and can load images. When you load an image, the vertical scaling for the display is automatically set so that the range of data values in the image spans the full range of grayscale values.

Image Browser accepts images in the Flexible Data Format (FDF), which is the type of data file created by the macros `svib` or `svsis`, described in the previous section "Saving Images from VNMR for Image Browser." Image Browser also accepts some types of images in the VNMR Phasefile format.

FDF Files

The FDF file is the file format of choice because all the information to describe the image is in the file and there is no directory structure necessary. An FDF file can be loaded by double-clicking, by selecting the file and pressing the Return key, or by selecting the file and clicking on the Load button.

VNMR Phasefiles

To retrieve images stored as VNMR phasefiles, select the directory that stores `datdir/phasefile` and `curpar`, and then select Load. For example, to analyze an image in VNMR in `exp3`, start Image Browser, select `exp3`, and load the image. (Note that double-clicking on the directory, or pressing Return after its name, opens that directory but does not load the image.)

Load All

Load All loads all the images in a directory. Images can either be FDF files or VNMR phasefile directories. If images have been loaded into all the Gframes and more images must be loaded, the next image is loaded into the first Gframe, and the process continues until all the image files have been loaded.

Storing Images

Images can be easily stored by using the *right* mouse button and selecting the Save item from the file menu selection list. The File Browser window is opened in Data Save mode, or the current File Browser window is changed to that mode. The initial File Browser directory is the directory in which Image Browser was started.

To store an image, choose a directory, a file name, and select the Save button. The image in the currently selected Gframe is saved. As a default, all data are saved as FDF files, but there are a number of alternate data formats that can be chosen to save files. Details are given in "Saving Files," page 105.

Using Graphics Tools

The Tools window is opened by selecting the Graphics Tools option from the Tools menu button on the control panel. The window opens, with the ROI Tools button (designated by an arrow) as the default.

The graphics tools in the Tools window can be used to support processing functions or used on their own for viewing images. The tools support:

- ROI manipulation
- Gframe manipulation
- Zooming
- Vertical scaling (scales the pixel display values to the data)
- Line ROI drawing
- Point ROI drawing
- Box ROI drawing
- Polygon or freehand ROI drawing
- Annotation

- Image math

To activate a tool, point to its button with the cursor and click the *left* mouse button. Once a graphics tool is activated, the corresponding function can be initiated in the graphics region with the *left* mouse button. Commands can be performed by opening the Properties menus with the *right* mouse button. Typical commands are load, save, or delete in the case of Gframes or ROIs, The commands zoom or unzoom are typical in the case of zooming.

Zooming

When Zooming is selected in the Tools window, a box cursor appears on all the selected Gframes. This function allows one image or a number of images to be magnified (zoomed) when zoom is selected from the Zoom Properties menu.

The zoom function can also be bound together across all selected Gframes so that when the cursor on one frame is manipulated, the cursors on all the selected frames change. Binding is enabled or disabled by selecting Bind from the Zoom Properties menu.

Image display can be performed either by Pixel Replication or by Pixel Interpolation. Once again, this is a property that can be selected from the Zoom Properties menu. If Pixel Interpolation is selected, a cubic spline interpolation is performed. Be careful when selecting Pixel Interpolation because interpolation takes significantly longer than replication and, unlike most selections in the Zoom Properties menu, this selection is used throughout Image Browser. Thus, any time an image needs to be updated for any reason, such as a change of size or vertical scale, it is done by pixel interpolation if this option is chosen.

Vertical Scaling

The vertical scaling function multiplies the data values by a number that maps them into the pixel values in the grayscale portion of the colormap (0 to 63 in the default `colormap.init` file). This value can either be entered by hand or by using the point-and-click method with the mouse.

To enter a value by hand, select the V-Scale entry from the V-Scale Properties menu. A window opens with the current default mapping, from data value to displayed intensity. A new scaling value or functional form can then be entered, and new settings are applied to all selected frames.

To enter a value using the point-and-click method, position the cursor within any image (the Gframe that holds the image does not need to be selected) and press the *left* mouse button. The intensity at that part of the image is used to select a vertical scale value. The brightest pixel within a few pixels of the cursor position is set to the top of the intensity range.

Vertical scaling also has a bind property. When Bind is in effect, all the images in selected frames are scaled to the same value as the image that you click on with the *left* mouse button.

Selecting the Gamma button from the V-Scale Properties menu allows corrections to be made according to the characteristics of a particular monitor.

Creating ROIs and Labels

ROIs are created by selecting the ROI type to draw, moving the cursor to the desired location, pressing the *left* button, and dragging out the desired ROI. ROIs can also be read in from a file. The Load button in the ROI Properties menu is selected with the *right* mouse button and dragged until a list of ROI files is displayed. When the desired file has been chosen, the ROIs stored in it are read in to all the selected Gframes. The ROIs are all placed

in the same locations in data coordinates. Their size and shape on the screen may differ, depending on the aspect ratio of the data and the size of the Gframe. This function is especially useful for calculating statistics on a number of files for the same region of interest.

When the size of an image is changed, the label font size remains fixed in terms of screen pixels. The left end of the text baseline is fixed on the data.

Storing ROIs and Labels

ROIs and labels are stored into and retrieved from the directory `$BROWSERDIR/roi`, or a subdirectory of `roi`, similar to the way Gframes are saved in the `gframe` directory (see "Storing and Retrieving Gframes," page 72). All the selected ROIs and labels are stored in the chosen file.

Note that ROIs and labels are not stored with an image when an image is saved.

Selecting ROIs

To select ROIs, click on the ROI Tools button  in the Tools window. This is the default mode of this window.

To select an individual ROI, position the cursor on or very near the ROI and press the *left* mouse button.

Selection of a number of ROIs can be done two ways:

- Use the *middle* mouse button to append one ROI after another to a selection list. However, this is method can be time consuming.
- Position the cursor to one side of the group of ROIs to be selected, and hold down the *left* button. Drag the cursor so it draws a selection box around the group of ROIs. Lift the *left* button. All the ROIs in the selection box are now selected.

ROIs are shown to be selected when their vertices are highlighted. When labels are selected, they show an underscore cursor at the end of the text.

Adjusting ROIs

To adjust the size or shape of an ROI, do the following steps:

1. Click on the  button in the Tools window.
2. Click the *left* mouse button near one of the ROIs vertices and hold down the button. The vertex jumps to the cursor position.
3. Drag the mouse, then release the button at the new desired position.

Moving ROIs

To move an ROI, do the following steps:

1. Click on the  button in the Tools window.
2. Click the *left* mouse button on an ROI, but AWAY from the vertex. For box, polyline, and polygon ROIs, click *inside* the area of the ROI. For lines or points, click NEAR the ROI.

   Clicking near a vertex activates the ROI adjusting mode. To avoid selecting a vertex and accidentally modifying an ROI, hold down the Shift key while clicking the mouse.

3. Use the mouse to drag the ROI, then release the button at the new desired position.

Obtaining Statistics from ROIs

The processing functions described in this section are used in conjunction with the graphics functions. Some of the processing functions use the ROI tools to obtain statistics or information from regions of interest within images.

The Statistics, Line, and Cursor functions are used on selected ROIs.

Statistics	Obtain statistics and histograms from regions of interest. It uses any type of ROI.
Line	Obtain distances, traces, and projections using a line ROI. It uses line or polyline ROIs.
Cursor	Obtain point intensities and distances between points. It uses point ROIs.

The Arithmetic, Math, Filtering, Histogram, and Rotation functions manipulate or process data. These functions are used on the whole image and selected Gframes.

Arithmetic	Add, subtract, multiply, divide images by other images or by a constant.
Math	Apply general math operations to images.
Filtering	Filter the data with a 3×3 or 5×5 pixel filtering functions.
Histogram	Use histogram methods to enhance the data.

Selecting Source and Destination Gframes

A source Gframe must be selected and, optionally, a destination Gframe can be selected. The first Gframe selected is the *operand*, the second frame added is the *operator*, and the third is the *destination* frame.To select frames, do the following procedure:

1. Select a source Gframe by moving the cursor into the desired Gframe and pressing the *left* mouse button; the Frame tool does not need to be active.
2. Obtain a destination Gframe by pressing the *middle* button when the cursor is positioned in the desired frame. In the case of the Arithmetic function, when two images are source frames, a third frame can be selected using the *middle* button as the destination frame.
3. After the frames have been selected, the Rotation function can be activated.

Rotation	Reflect images and rotate in 90° increments. This function operates on the images in the selected Gframes.

Using the Movie Mode

A number of images can be chained together and sequentially displayed to produce an animated image by using the Movie mode. The movie mode is started by selecting the Movie button in the control panel. This opens a Movie Control panel. Before the movie can be run, the desired image frames for the movie must be selected. These frames are designated by means of a “playlist.” A playlist is a list of the image files that make up a movie. It can be saved and retrieved, so the movie need not be specified every time.

Generating a Playlist

Once a Movie Control panel appears, a playlist can be started by selecting the Load Frames button, which opens an empty Playlist window and a Movie Frame Loader window. Now files can be browsed and images can be loaded into the playlist. Put entries into the playlist by selecting the Load button or Load All button from the Movie Frame Loader menu. When an image is loaded into the playlist, it is also displayed in the currently selected Gframe. Entries are always inserted in front of the currently selected line in the playlist.

To delete entries from the playlist, choose an image name, then select Delete.

When a playlist has been completed, it can be saved as an FDF file so that it can be retrieved at a later time. A playlist file consists of the fully qualified names of all the image files used in the movie. Because there is no data associated with an FDF playlist file, the file is in standard ASCII format and can be edited if desired.

Be aware that the files are specified as fully qualified names. Therefore, if the image files are moved or if they are found on different mount points on different workstations, they might not be found when the playlist is later loaded. However, using the fully qualified name does allow more user flexibility with a personal directory structure when storing images.

Playing the Movie

After the playlist has been constructed, play the movie by selecting either Forward or Reverse in the Movie Control panel. The movie is played in the currently selected Graphics frame. Note that when the vertical scaling or image size is changed, the movie runs more slowly the next time through the loop. The slower speed occurs because the program is taking advantage of the pixel buffering capabilities of the X Window System and generating pixel files for display. The movie can be stopped at any time, and another graphics frame can be selected, and the movie can be started in the new Gframe.

Changing the Frames/sec entry alters movie speed. To change movie speed, stop the movie, enter a new frame speed number, and restart the movie. Frame speed is also monitored so that it can be determined whether or not the current environment can support the requested speed. While running over the network, the Speed indicator does not always clearly indicate problems, but any kind of erratic movement of the indicator should signal that there is a problem. A subsection of the playlist can be played by using Start and Stop. Pictures can be stepped through one at a time by using Current.

Zooming and Vertical Scaling

Zooming and vertical scaling can be performed on images. Images can be zoomed and the zoomed region animated by stopping the movie and selecting Zoom in the Tools window. Interpolation can be used when zooming, but it makes the startup time much longer because each image has to be interpolated to generate the pixel image to display.

Vertical scaling can also be used. One image in the movie can be scaled or all the images in the movie can be scaled if Bind is selected.

A movie frame can contain ROIs, but drawing an ROI on one movie frame does not affect the other frames in the movie. To put the same ROI on all frames in a movie, step through the movie frame by frame and load the desired ROI file into each frame.

Using Keyboard Accelerators

Since it can be inconvenient to switch back and forth between different graphics tools, a few commonly used functions can be performed by using various key combinations. The following keys work ONLY when an ROI graphics tool is selected.

> If any text annotation is currently selected, pressing a key causes text to be added to the label. To prevent this action, hold down the Control key while using the keyboard accelerators (or deselect any text annotation).

z (lowercase z) zooms OUT on the image under the cursor by the same factor that Z zoomed in.

C (capitalized or lowercase) moves the image under the cursor to the center of the point under the cursor in the Gframe.

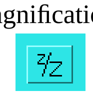
Shift-Z (capitalized Z) zooms IN on the image pointed to by the mouse cursor. The point indicated by the cursor is moved to the center of the Gframe unless such a move would result in blank space between the image and the frame. By default, each time that you press Z, the image scale is enlarged by a factor of 2.

Changing Zoom Magnification

You can change zoom magnification with the Image Browser command `zoom_factor`. As an example, to change magnification by a factor of 1.414, do the following steps:

1. Click on the Macro button.
2. Click the On button in the Record field to record the change.
3. Enter **`zoom_factor(1.414)`** on the Name line.
4. Click on the Execute button.

You can also change zoom magnification by doing the following steps:

1. Select the Zoom button  in the Tools window.
2. Click on the Zoom Properties button with the *right* mouse button and select the Zoom factor option.
3. In the Zoom magnification factor window, enter the desired magnification factor, as shown in Figure 28.

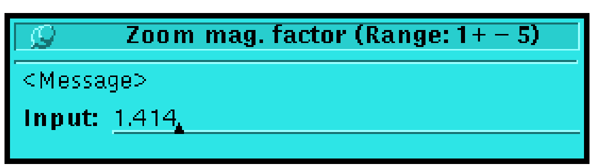


Figure 28. Zoom Magnification Factor Window

4.3 Graphics Tools

This section is a reference about the Tools window displayed when the Tools button in the Image Browser control panel is selected.

Figure 29 shows the Tools popup window. Only one graphics tool can be active at a time (to prevent confusion over mouse button use). The Tools window contains a set of graphics tools to create objects, manipulate objects (or an image inside an object), and draw annotation on images. Choose a tool by clicking the *left* mouse button for the desired tool.

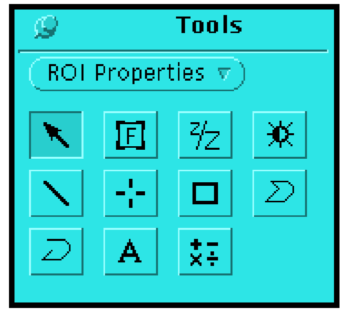


Figure 29. Tools Window

In addition to the buttons for tools, there is a Properties button that activates a menu, listing several commands and options. The choices of these menus can be an action to save, load, process, popup another window, etc., depending on the individual function of the tool selected.

Frame Properties Menu

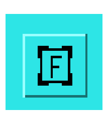
The frame properties menus can be "pinned" to the screen desktop by selecting the pushpin icon in the top left-hand corner of the menu. Pushpins allow a group of functions to be easily accessed without first selecting the corresponding graphics tool. For example, with the Zoom Properties menu pinned, the Pixel Interpolation button can be toggled at any time without having to go into zoom mode.

Be aware that when pinned menus are used, some menu choices display a list of file names used to retrieve ROIs, filters, etc. These submenus are not updated if, for example, a new ROI is stored. The submenus list the files that existed when the menu was pinned. To update the menu, close it by selecting the pushpin, and then pin a new menu.

Graphics Frame Tools

The following sections describe the functionality of tools. Use of the mouse to select, create, move, or resize is not discussed here (see the *OpenWindows User's Guide* for mouse use related to graphics).

Frame Tool



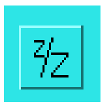
The Frame tool is used to create a graphics frame (Gframe). A Gframe is used to indicate the position and size of an image on the screen. An image can only be displayed inside a Gframe. The number of Gframes is limited only by computer memory. When this tool is selected, frames can be created and resized in the graphic region with the mouse.

The Frame tool properties menu consists of the following options:

Split Selected Frames	Splits each selected graphics frame into an array of smaller frames. If there are no Gframes in the graphics region, the entire region is split into the selected matrix of frames. Select the desired $n \times m$ entry from the submenu to make an array of n rows by m columns. Or select Other to split frames into an arbitrary number of rows and columns.

Delete	Deletes all graphics frames, all selected graphics frames, or all unselected graphics frames.
Clear	Clears all graphics frames, all selected graphics frames, or all unselected graphics frames.
Select All Frames	Selects all graphics frames.
Load Frame Layout	Loads graphics frames from a file in the directory `$BROWSERDIR/gframe` or a subdirectory.
Save Frame Layout	Saves graphics frames into a file in the directory `$BROWSERDIR/gframe` or a subdirectory.

Zooming Tool



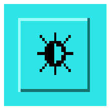
The Zooming tool is used to select a portion of an image to be expanded. Box cursors are displayed on all the currently selected Gframes. The cursors are XORed to the image.

The zooming tool menu consists of the following zoom properties:

Zoom	Zooms selected images.
Unzoom	Unzooms selected images.
Bind//Unbind	Adjust the zoom lines to all selected images. The zoom lines are the lines that control the portion of images to be zoomed.
Zoom Tracking	Controls the real-time tracking of the zoom line positions in other selected Gframes when zoom "binding" is enabled. You can set the maximum number of tracking frames. If you set the number to 0, only the zoom lines in the Gframe in which the mouse is dragged will change in real time. When you release the mouse button, the zoom lines in all selected frames will snap to the new position. If you set the number of frames to a number, *n* (that is less than the number of selected Gframes), only the first *n* selected Gframes will track in real time.
Zoom Factor	Allows you to set the number that controls the zooming magnification factor. See the "Using Keyboard Accelerators," page 79 for more information.
Cursor Tolerance	Controls the sensitivity of the cursor for the zoom lines. This specifies how close the mouse cursor must be to a zoom line to select it.
Pixel Interpolation/ Pixel Replication	When Pixel Interpolation is displayed in the menu, it means that pixel replication is being used to expand the size of the images to display on the screen—not just when zooming, but at any time an image is redisplayed. If Pixel Replication is displayed, it means that pixel interpolation is currently selected, and cubic spline interpolation is used to display the images. Note that the pixel interpolation takes much longer than pixel replication.

Some Zoom functions are available by using keyboard accelerators. See "Using Keyboard Accelerators," page 79 for more information.

Vertical Scale Tool



The Vertical Scale tool is used to adjust the vertical scale of an image. When this tool is active, frames must not be selected or deselected with the mouse, because clicking on an image changes the displayed intensity. However, a frame does not have to be selected in order to adjust its vertical scale with the mouse; any image that you click on is rescaled.

There are three methods to adjust vertical scale:

- *Click the left mouse button on the image* – The program finds the maximum data value within a 10-pixel square box centered on the cursor, and the vertical scale is adjusted to put this pixel at the top of the grayscale.

  Hold down the Shift key while clicking the mouse to put the zero data value at the bottom of the grayscale.

  Hold down the Control key to force the image clicked on to be autoscaled. In this case, it does not matter where you click on the image.
- *Click and drag with the middle button in the Graphics Region* – This method operates on all selected Gframes, and adjusts both the brightness and contrast. Dragging the mouse left or right makes the displays darker or lighter, respectively; dragging down or up decreases or increases the contrast. While you drag the mouse, a preview of the new settings is displayed by modifying the display's color map. When you release the *middle* button, the original color map is restored, and all the selected frames are rescaled. All images will change while you are dragging the mouse, but only the selected images will be permanently changed. Also, the preview feature only works well if the V-scale mapping function is nearly linear.
- *Open a popup window to enter the desired vertical scale value.*

The Vs Prop (vertical scale properties) menu has three choices, as shown in Figure 30:

- V-scale changes the mapping of data values to the colormap index;
- Gamma changes the pixel values in the colormap itself. Gamma correction is to be used only to correct the image display of a particular monitor.
- Unbind (or Bind) sets whether only one image or all selected images are rescaled. For details, see "VsProp Menu: Unbind or Bind," page 87.

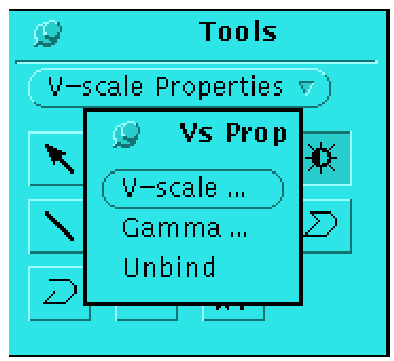


Figure 30. Vertical Scale Properties Window

V-scale adjustment is to be used to emphasize particular intensity ranges in an image. Because gamma corrections are made in the common Image Browser colormap, they apply to all images being displayed; the V-scale adjustments might be different for each image. The V-scale choice is described in the next section; gamma is covered starting in "VsProp Menu: Gamma Correction," page 85.

Vs Prop Menu: Vertical Scaling

The V-scale choice on the Vs Prop menu displays the Vertical Scaling window in which vertical scaling can be set, as shown in Figure 31. The range of data values to be mapped to grayscale values and the form of the mapping function can both be changed. Any changes in vertical scaling are applied to all the selected Gframes. Changes to the mapping function are also applied to any new images when they are loaded, but the data range is scaled to match the data in the particular image.

The graph at the bottom of the Vertical Scaling window is a plot of gray level as a function of data value. (The “gray level” corre-sponds to the index into Image-Browser’s colormap. The intensity of the screen pixel as a function of colormap index is set by the Gamma Correction window, discussed in “VsProp Menu: Gamma Correction,” page 85.)

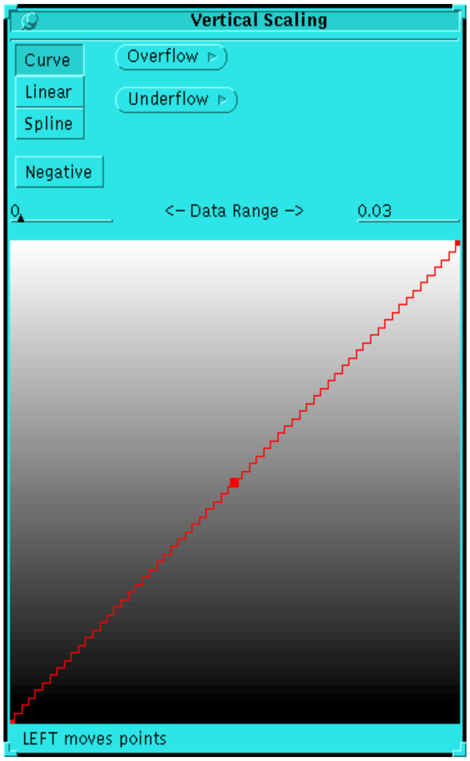


Figure 31. Vertical Scaling Window

Data Range

The range of data values to map to the full range of gray values is set by the two type-in fields labeled Data Range. The data values are plotted linearly along the horizontal axis, between the values in the Data Range fields. (You must press the Return key in at least one of the fields for the changes to take effect.)

Mapping Function

The shape of the mapping function is selected by the buttons at the upper-left of the Vertical Scaling window. The mapping function translates the data value in a pixel to a corresponding grey level.

In the following discussions, normalized variables are used: *x* and *y*, for the data, and for the grey level values, *d* and *g*. These variables are defined as

$$x = \frac{d - d_{min}}{d_{max} - d_{min}} \quad \text{[Eq. 21]}$$

and

$$y = \frac{g - g_{min}}{g_{max} - g_{min}} \quad \text{[Eq. 22]}$$

Therefore, both *x* and *y* vary from 0 to 1. Note that with the appropriate gamma correction (discussed in the next section), the actual screen intensity will vary exponentially with *y*.

For any type of mapping function, the Negative button can be selected to invert the intensity scale; that is, the minimum grey value will be white and the maximum, black.

Curve Mode

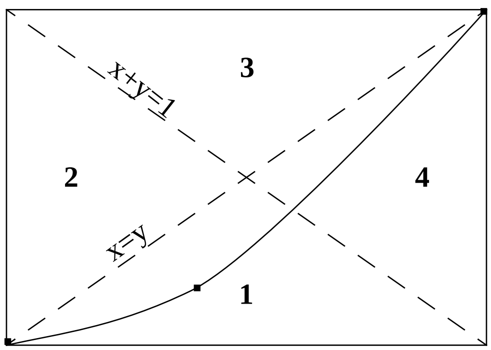
The type of mapping function is selected by the buttons at the upper-left of the Vertical Scaling window. The default is curve, which provides a flexible functional form that includes power functions and a close approximation to exponential functions. The two parameter family of curves are controlled by moving the curve's control point around with the *left* mouse button. The left and right ends of the line can also be moved up and down. The form of the function depends on which regions of the graph the control point is in.

If the control point is in region 1, as shown in the Figure 32, the following equation shows the defining function for these curves:

$$y = \left(\frac{x}{x - ax + a}\right)^{b} \qquad \text{[Eq. 23]}$$

where *a* and *b* are the two adjustable parameters. The ranges of *a* and *b* are:

$$a > 0,\ 1 \le b \le 10 \qquad \text{[Eq. 24]}$$



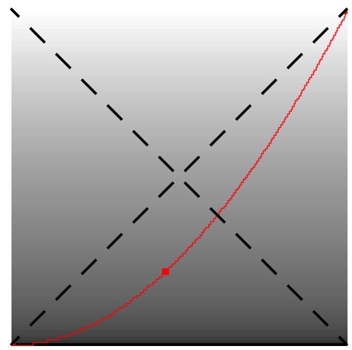


Figure 32. Curve Control Point

Note that if $a = 1$, this reduces to a power function, which is the case if the control point has $x = 0.5$. If the control point is in region 2, the curve is reflected through the $x = y$ line. This family of curves includes power functions of the form

$$y = x^{1/b} \qquad \text{[Eq. 25]}$$

which applies if the control point is on the $y = 0.5$ line. If the control point is in region 3 or 4, the curves for regions 2 or 1, respectively, are reflected through the $x + y = 1$ line.

Linear Mode

The linear mode allows the user to specify a piecewise linear function that passes through all of the control points. Any additional number of control points can be added by clicking the *left* mouse button anywhere on the canvas away from an existing control point. Control points can be deleted by clicking on them with the *middle* mouse button.

It is best to avoid large discontinuities in the slope of this function at the control points. Due to the characteristics of human vision, these discontinuities can make a surface that increases smoothly in intensity across a picture appear to be non-monotonic in intensity! For this reason, the third mode might be more useful.

Spline Mode

The spline mode is like linear mode, except that a spline curve is drawn through the control points instead of straight lines. It is also coupled to the linear mode in that the two modes

share the same control points; changing the control points in one mode also changes them in the other.

The spline function used here interpolates between control points with cubic polynomials, arranging that the slopes match at the control points. The final curve is continuous up to the second derivative. At the endpoints second derivative is forced to zero—the defining condition for the so-called “natural” cubic spline.

Underflow and Overflow

The Underflow and Overflow menus control how data values outside of the domain of the mapping function are displayed. The default is Off, meaning that data values less than the “minimum data value” ($x < d$) are displayed the same as $x = d$, and that data values $x > D$ are displayed the same as if $x = D$. The menus offer a number of alternative color choices for such values.

VsProp Menu: Gamma Correction

The Gamma choice in the Vs Prop menu opens the Gamma Correction window, shown in Figure 33. The primary purpose of gamma correction is to make optimal use of the limited number of grayscale steps in Image Browser’s colormap. A secondary purpose is to compensate for any unusual nonlinearities in the monitor’s displayed intensities. Compensation allows images to appear the same with identical scaling on any monitor — once gamma correction has been done. For a properly adjusted monitor, minimal gamma correction should be necessary.

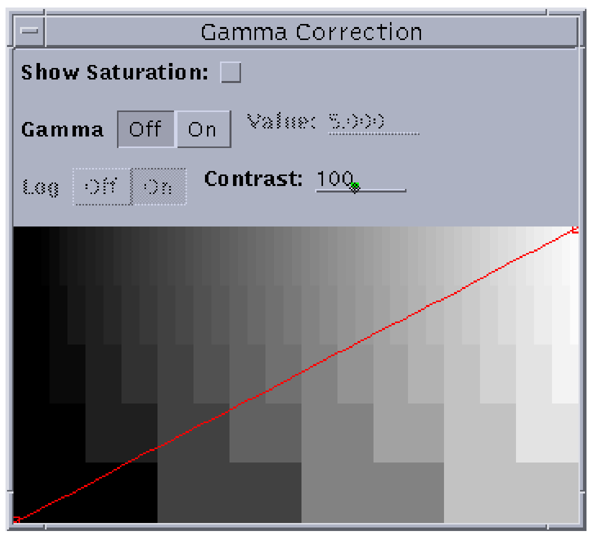


Figure 33. Gamma Correction Window

The Gamma Correction window has a plot at the bottom that graphs the pixel value (between 0 and 255) against the index into the grayscale portion of Image Browser’s colormap. (Pixel value is actually a color that has a red, green, and blue value, but the grayscale always uses the same value for each color.) The graph background is painted with several rows of gray steps to demonstrate the current gamma correction. The top row shows every step in the grayscale ramp; the second row, every other step; the third row, every fourth step; and so on. (It appears to the eye that each ramp step is shaded from a lighter gray on the left to a darker gray on the right. This is an *optical illusion*, which can be seen by masking out the surroundings of one of the steps with a paper frame.)

Ideally, no steps should be visible anywhere in the top row, but, if the Image Browser colormap is fairly small (like the 64-step default for 8-bit color machines), they can be easily seen. The goal of gamma correction then becomes to make each intensity step equally apparent to the eye. For a short grayscale ramp, this process can involve looking only at the top row of steps. For a larger ramp, the second or third row might need to be

examined. (The size of the grayscale ramp is set in the `colormap.init` file in the `$BROWSERDIR` directory. See “Initialization Directory,” page 68 for details about Image Browser initialization.)

Before adjusting the gamma correction, adjust the monitor. Some monitors have no easily accessible brightness control; therefore, monitor adjustment should be performed by a service person.The most common problem with monitor adjustment is that the black level is set too dark, making everything near the bottom end of the intensity scale appear black. Set the “brightness” control (labeled ☼ on some monitors) just low enough so that the blackest level, at the left of the grayscale ramps (pixel value 0), is indistinguishable from the unscanned black background at the edge of the monitor screen. To accomplish this adjustment, it might be convenient to move the Gamma Correction window slightly off the bottom of the screen, so that the bottom row of steps directly merges with the unscanned margin.

Once monitor brightness has been adjusted correctly, the perceived prominence of the intensity steps in the Gamma Correction window should be roughly equal with no gamma correction.

The gamma correction described in the following paragraph is still effective on a poorly adjusted monitor; although, if the brightness is set too high, there is no way that the lowest gray level can be made entirely black.

Two forms of gamma correction are available. When the Gamma and Log switches are both set to ON, Image Browser attempts to make each step in the colormap index an equal step in the log of the screen intensity, which assumes that the screen intensity is described by a function of the form:

$$I = I_0 + V^{\gamma} \qquad \text{[Eq. 26]}$$

where I is the intensity, V is the voltage (proportional to the pixel value), γ is a characteristic of the monitor (equal to about 2.5), and I_0 is the background intensity due to room illumination or poor adjustment of the monitor.

The Value field next to the Gamma switch controls the value of γ used in the above equation. The Contrast field, next to the Log switch, specifies the value of the ratio of maximum to minimum displayable intensities, in effect, I_0 in the previous equation. Normal values for a properly adjusted monitor are 50 to 100 for I_0 and about 2.5 for gamma. If the monitor brightness is not properly adjusted, it is still usually possible to get a good fit by adjusting γ; the function is relatively insensitive to the Contrast value.

When the Gamma switch is on, a “control point” is displayed near the middle of the gamma correction curve. This control point can be dragged with the *left* mouse button to adjust the Gamma value. The Contrast value can only be changed by typing a new value in the text field.

If the Gamma switch is ON and the Log switch is OFF, correction is made for equal steps in intensity, according to the formula $I = V^{\gamma}$

This correction is not ideal, but it might be useful for emphasizing the contrast in some region of the colormap, which could normally be done with the V-scale function instead.

Saturation

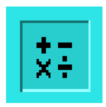
If the Show Saturation button at the top of the Gamma Correction window is selected, pixels that are mapped to the maximum grayscale value are displayed yellow. This button should normally be left off; the Overflow button in the Vertical Scaling window essentially performs the same function.

VsProp Menu: Unbind or Bind

The last choice in the Vertical Scaling Properties menu is Bind or Unbind:

- If Unbind is displayed, the current mode is bound, and the images in all selected Gframes are rescaled the same as the one you click on.
- If Bind is displayed, it means that the current mode is unbound. Clicking the *left* button on an image affects only that image.

Math Tool

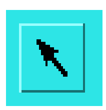


The Math tool is used in conjunction with the Image Math processing window to enter Gframe numbers in mathematical expressions. Position the mouse inside a Gframe and press the *left* mouse button to insert the Gframe number in the math text window. The Math Properties menu has no choices in it. Chapter 5, “Image Browser Math Processing,” has more information about this tool.

ROI Tools

The following sections describe the tools that draw and modify regions of interest (ROIs).

ROI Selector



The ROI Selector tool is used to select and adjust any of the ROIs. It is the default mode of the graphics tools. After any ROI has been drawn, a graphics tool reverts to the Selector tool. In this mode, both ROIs and Gframes can be selected or deselected in the graphics region. The *left* button selects an object while deselecting all other objects of the same type. The *middle* button toggles the state of an object.

The object selected is chosen according to a priority hierarchy:

1. If the mouse pointer is inside an ROI, near a line or point ROI, or near text, the corresponding object is selected. If there is more than one qualifying object, only the most recently created object is selected.

2. If the mouse pointer is outside any ROI but inside a Gframe, the frame is selected.

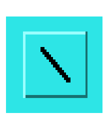
Table 6 lists the ROI properties of the ROI Selector tool.

ROI Drawing Tools

The following tools are used for drawing various types of ROIs.

Normally, after an ROI is drawn, a graphics tool reverts to the ROI Selector. To prevent this reversion (when you are drawing a series of similar ROIs), hold down the Shift key while drawing each ROI. Before you draw the last ROI, release the Shift key to allow the graphic tool to revert to the Selector.

Line ROI Tool



The Line ROI tool draws a straight line segment ROI. Line ROIs are used in the Line Data processing function. It is also possible to obtain statistics from a line ROI. The points included in the statistics are the points along the line.

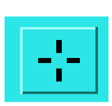
To draw a line after the tool is selected, position the cursor at one of the desired endpoints, press the *left* mouse button and drag the cursor to the other end point. As

Table 6. ROI Selector Tool Properties

Property	*Function*
Delete	Deletes all selected ROIs.
Load	Loads ROI tools from a file in the directory `$BROWSERDIR/roi`.
Save	Saves ROI tools to a file in the directory `$BROWSERDIR/roi`.
Color	Changes the ROI tool color. The colors of all the selected ROIs and labels are changed. Any new ROIs and labels are also drawn in the selected color.
Font Size	Sets size to use for the next annotation entered: 10 pt., 12 pt., 14 pt., or 19 pt. Size cannot be changed once the label has been created.
Cursor Tolerance	Adjusts the cursor sensitivity: how close the mouse cursor must be to an ROI vertex to select that vertex.
ROI Bind/Unbind	If binding is on (Unbind label shows in menu) whenever a new ROI is drawn, identical ROIs are drawn in all the selected Gframes. All of these ROIs can be operated on as a group. They are considered members of the same group solely because they are all identical; Image Browser does not store any information about whether ROIs were created as a group. When ROI binding is on, all identical ROIs are operated on as a group. If binding is turned off and one of the ROIs is modified individually, it is no longer modified along with the others when binding is reactivated. All identical ROIs are considered part of the group, the Gframes that they are in do not have to be selected once the ROIs have been created. When ROI binding is on, all ROI modifications (moving, resizing, or adding or deleting polygon vertices) are applied to all ROIs in a group. While a group of ROIs are being created or modified, they might not appear exactly identical, because integer arithmetic is used to translate mouse actions in one graphics frame to roughly equivalent mouse actions in another frame. This effect can be particularly noticeable when the "master" frame is much larger than the "slave" frames. Polygons, in particular, can have fewer vertices in smaller frames. However, when the creation or modification is completed, all the slave ROIs are replaced with copies of the master ROI.
Tracking	Controls the real-time updating of the "slave" ROIs when ROI binding is enabled. The maximum number of tracking ROIs is set by the user. If set to 0, only the ROI on which the mouse operates directly changes in real time, but when the mouse button is released, all the ROIs in all the group snap to the new configuration. In general, if set to a number, *n*, less than the number of selected ROIs, only the ROIs in the first *n* Gframes track in real time.

the cursor is being dragged, the line is drawn in the active ROI color (purple, by default). When the *left* button is released, the completed line appears in the selected ROI color. The Line ROI tool has the same ROI Properties menu choices as the ROI Selector tool.

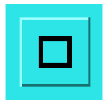
Point ROI Tool



The Point ROI tool draws a point or cursor ROI. Cursor ROIs are used in the Cursor Data processing function, and can also be used by the Statistics processing function.

To draw a point after the tool is selected, position the cursor at the desired point and click the *left* mouse button. A point ROI appears and is selected. This tool has the same ROI Properties menu choices as the ROI Selector tool.

Box ROI Tool



The Box ROI tool draws a rectangular ROI. It is used in the Statistics processing function.

To draw a rectangular ROI after the tool is selected, do the following steps:

1.Position the cursor at one of the desired corner coordinates.

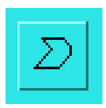
2. Press the *left* mouse button and drag the cursor over the desired region of interest area.

   As the cursor is being dragged, a rectangle is drawn in the active ROI color.

3. Release the *left* button.

   The completed rectangle appears in the selected ROI color. This tool has the same ROI Properties menu choices as the ROI Selector tool.

Polygon ROI Tool



The Polygon ROI tool draws a freehand or polygon ROI. It is used in the Statistics processing function. The Polygon ROI tool has the same ROI Properties menu choices as the ROI Selector tool.

To draw a freehand ROI after the tool is selected, do the following procedure:

1. Position the cursor at the starting location along the boundary of the desired region of interest.

2. Press the *left* mouse button and slowly drag the cursor along the edge of the region of interest area.

   As the cursor is being dragged, a line is drawn (in the active ROI color) following the movement of the cursor.

3. Release the *left* button and move the mouse to connect the cursor to the last defined point; a straight line appears.

4. Press the *left* button to define the next point.

   Be careful about moving the cursor before the line is closed because that cursor location is included as part of the closing position; however, this shouldn't cause much concern because each freehand or polygon segment can be adjusted after it has been created.

To draw a polygon ROI, do the following procedure:

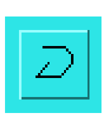
1. Move the cursor to each desired vertex and click the *left* button.

   After the first click, a straight line follows the cursor and at each cursor location where the mouse *left* button is clicked a vertex is placed.

2. Click the *middle* button to close a freehand or polygon ROI.

   A straight line is drawn between the last and first vertices, and the completed ROI appears in the selected color.

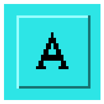
Polyline ROI Tool



The Polyline ROI tool functions the same way as the Polygon ROI tool except that the last line segment closing the polygon is not drawn. It can be used in the Statistics processing function, in which case it defines the union of all the

line segments in the polyline. It can also be used in the Line Data processing function. It also provides a way of drawing arbitrary lines on the image for annotation.

Annotation Tool



The Annotation tool is used for text annotation. After selecting the tool, position the cursor at the desired spot and click the *left* mouse button. An underscore cursor appears at the marked location, indicating that the label is selected and ready to accept typed input. Typed characters are always added to the end of the annotation field; they cannot be inserted into the middle of a string. The label can be selected and moved to other locations at any time. If more than one label is selected, typed input is appended to all of the selected labels.

4.4 Data Processing

Image Browser can process multiple images. Some operations can be simultaneously applied to several images, and some can only be applied to one image and then repeated on other images. For example, image rotation can be applied to several images at once, but it is not suitable to simultaneously add several sets of two images. Therefore, the decision to simultaneously apply a specific operation to several images depends on the nature of the operation.

To simultaneously apply an operation to several images, select several graphics frames that contain images to be processed. Of the processing functions, only image rotation can be done simultaneously on multiple images.

Some operations, such as adding two images, might need more than one data source. To add two images, select two sources (graphic frames that contain images) and a graphic-frame destination. Because no more than one destination can be selected, the last selected graphic frame is always the destination. To add a constant to an image, select a source frame and a destination frame.

Be aware that the last selected frame is always the destination. For example, adding two images with one selected frame or more than three selected frames is not allowed. However, adding two images with two selected frames indicates that the image result (destination) should overwrite the second source image (the second image selected).

When using Image Browser, remember that statistics are performed on the actual image data pixels, not on the displayed pixel values. That is, enhancing an image for viewing by using the Contrast tool or the Vertical Scaling Graphics tool does not change the statistical values. However, processing functions (filtering, histogram enhancement, etc.) change the data values and hence the statistics from those images.

Statistics

Statistics are always performed on ROIs, not on images as a whole. They can be performed on one ROI or a number of ROIs. The ROIs can all be on one image or across a number of images. If statistics are performed on one ROI, a histogram is displayed along with the statistics. If statistics are performed on a number of ROIs, a graph is displayed with a selection of axes. Statistics are run for all selected ROIs.

To open a statistics window, choose the Process button with the *left* mouse button. Press the *right* button to see a selection of processing options.

Updating Statistics

To update ROI statistics, choose the Update option and use either the *left* or *right* mouse button to update statistics:

- Press the *left* button on the Update option to just update the statistics and the graph.
- Press the *right* button to choose one of the following options for when to automatically update statistics:

Now	Same as pressing SELECT. The statistics are updated, but the mode is not changed. This is the default selection.
Manual	Statistics are only updated when the Update button is pressed, or when ROI Statistics are selected from the Process menu.
Auto (On ROI Change)	Statistics to be updated whenever an ROI is selected or deselected, or when an ROI is moved or modified. Updates only take place after a change is completed, not as an ROI is being moved around. This is the default mode.
Auto (On ROI drag)	Same as Auto (On ROI Change) except updates are done in real time as an ROI is being moved or resized. This mode can significantly slow down response time, especially when a large ROI is modified or many ROIs are selected.

Setting Histogram Display Limits

When statistics are requested for one ROI, a window with a histogram of intensities similar to Figure 34 is opened. A full complement of statistics is displayed for the ROI: minimum, maximum, median, mean, and standard deviation of pixel intensities; and ROI area and volume.

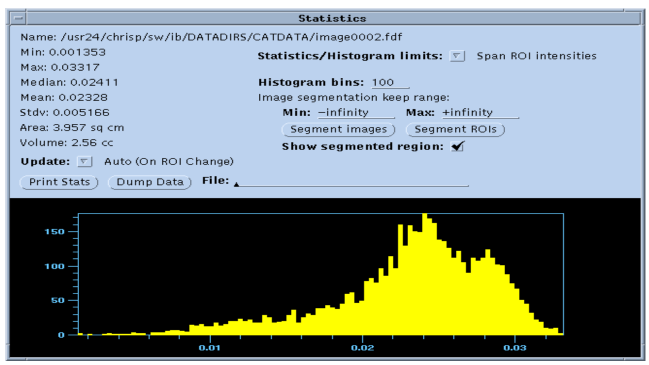


Figure 34. Statistics Window with One ROI

Only pixels with intensities between the set limits are included in the histogram or in the statistics calculations. So, for example, the calculated volume decreases as the limits are imposed.

The Statistics/Histogram limits menu offers the following ways to set histogram limits:

Span ROI Intensities	Sets the histogram limits to the maximum and minimum intensity values in the ROI. This option is equivalent to no limits on the pixel intensities included in the statistics and volume calculations.
Span Image Intensities	Sets the histogram limits to the maximum and minimum intensity values in the image. The median value might change when using this span, as opposed to Span ROI Intensities, because of the finite data binning used to calculate the median. The real difference is in the histogram display appearance.

Match Segmentation Limits	Uses the Image segmentation keep range defined by histogram cursors whose values are displayed by the Min and Max entries (see Figure 34). The default range limits (–infinity, +infinity) are the same as those in Span ROI Intensities. In this mode, statistics values depend on segmentation limits, because the only pixels being used to generate statistics are pixels whose intensity values lie within the image segmentation keep range. Narrowing the segmentation limits decreases the calculated area when statistics are updated.

Specifying the Intensity Range

Select the User Specified option to enter limits for the intensity range of the pixels selected for statistics and histogram display.

To get greater resolution in the histogram, modify the Histogram bins entry. A region with finer resolution can expanded and a search for intensity patterns within a large grouping of intensities can be run.

To update the histogram and the statistics after the limits have been changed, or the number of bins has been changed, select the Update option.

Segmenting Images

You can perform simple image segmentation functions by using the histogram display in the Statistics window. After a histogram is displayed, position the cursor within the Histogram window and press the *left* mouse button to draw the "min" cursor in the window. All intensities below the value at the cursor are unused or zeroed in any of the segmentation functions. Press the *left* mouse button again to draw another cursor. All voxels with intensities outside the intensity region delimited by the two cursors are segmented out of the image.

Define the segmentation range by entering the desired ranges into the Image segmentation keep range Min and Max fields. Note that these values also change as the cursors are moved around in the histogram. Move the cursors by holding down the *left* mouse button and "dragging" the cursors. Delete the segmentation cursors by clicking on them with the *middle* mouse button.

Select the Show segmented region box to interactively adjust the segmented region. This option updates the color map and places blue pixels wherever a pixel lies below the desired intensity range, and places orange pixels wherever a pixel lies above the desired intensity range. (These colors can be changed in the `colormap.init` file.) Because this option is changing the color map, all the images in the graphics region are affected, not just the image containing the ROI. However, the segmentation display is only correct for images with the same vertical scale as the image with the selected ROI.

Once the desired intensity ranges have been picked, the image can be segmented by zeroing all the pixels in the image outside the selected intensity range. Alternatively, the ROI can be segmented within the image by zeroing all the pixels outside the ROI and zeroing all the pixels outside the selected intensity range within the ROI. The first or second action can be taken by selecting Segment Image or Segment ROIs, respectively. When Segment ROIs is selected, all selected ROIs are segmented.

Once an image has been segmented, it cannot be restored except by reading it back in from its original file. So if permanent segmentation of an image is not wanted and only statistics from the defined segmented region are instead desired, choose Match Segmentation Limits in the Statistics/Histogram limits field.

Making Volume Measurements

Use the Image Segmentation features to make volume measurements over one image or over a number of multislice images. The volume field in the Statistics window is calculated as the image area within the ROI times the slice thickness of the image. When using the Match Segmentation Limits, only the voxels with intensities within the segmented intensity region are used in the volume calculations (which is also true for the area and other calculated statistics).

Graphical Display

When more than one ROI is selected, and statistics are selected, a graph similar to Figure 35 is displayed with selectable items for the *x* and *y* axes. The graph provides a quick look at information from processing on regions of interest.

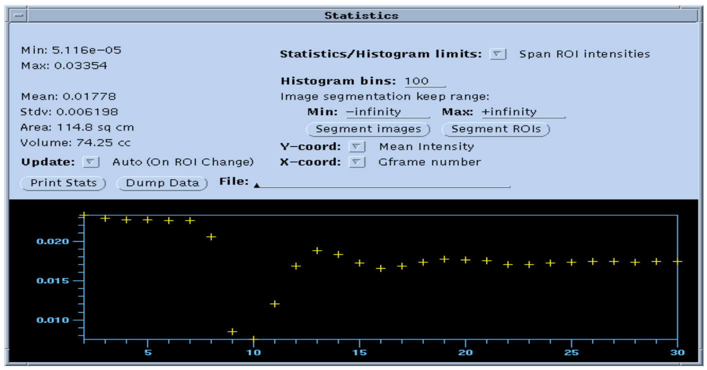


Figure 35. Statistics Window with Multiple ROIs

In the graphics display, the histogram limits are displayed, because these can still be used to segment regions when gathering statistical information from multiple ROIs. The statistics displayed on the left side are for the sum of all the ROIs. For example, if there is no overlap, the area is just the sum of the areas for all the ROIs. If any of the ROIs overlap, some of the pixels are counted twice in the statistics.

Volume calculation is a special case. If a calculation is labeled simply as Volume, it is just the sum of the individual ROI volumes. However, if a calculation is labeled 3D-Volume, it is calculated by accounting for the difference in ROI slice positions and interpolating the cross-sectional ROI area between slices.

The calculation is illustrated in Figure 36, in which the cross-sectional area of the volume-ROI is calculated by linearly interpolating the ROI area between slices. The ROIs are assumed to lie at the center of the slices. The top and bottom “caps” are half as tall as the slice thicknesses.

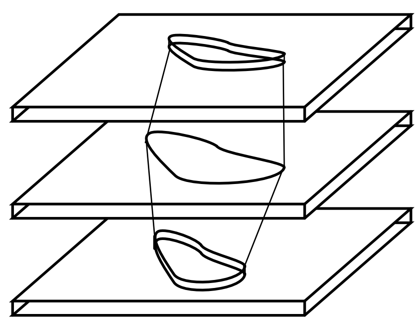


Figure 36. 3D Volume Calculations

Each axis of the graph can be chosen by selecting an item from the Y-coord list and the X-coord list using the *right* mouse button. The following items can be selected from each list:

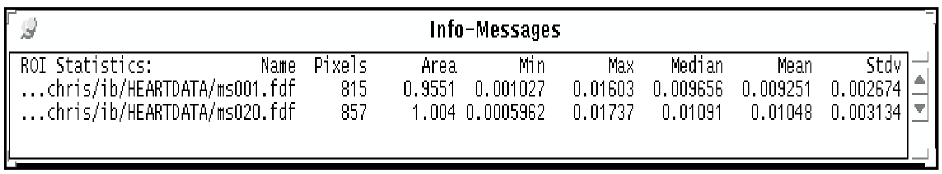
Y-coord	Area, volume, integrated intensity, mean intensity, median intensity, minimum intensity, maximum intensity, and standard deviation (SDV) of intensity.
X-coord	ROI number, slice location, user parameter, area, volume, integrated intensity, mean intensity, median intensity, minimum intensity, maximum intensity, and standard deviation (SDV) of intensity.

The user parameter can be time information for T_1/T_2 data or any other information. However, the field must be put into the FDF file header. Normally, it is a VNMR parameter dumped out into the FDF file by the `svib` macro.

If the Y-coord or X-coord selection is changed, the display is updated automatically. However, any change in the limits or changes to the ROIs themselves are not reflected until the Update button is pressed.

Statistics Output

If desired, statistics values can be written to a file for further processing by using the Print Stats button. Print Stats writes the formatted statistics in the Info Messages window. Figure 37 shows the output from two selected ROIs generated by Print Stats.


Info-Messages

ROI Statistics: Name	Pixels	Area	Min	Max	Median	Mean	Stdv
...chris/ib/HEARTDATA/ms001.fdf	815	0.9551	0.001027	0.01603	0.009656	0.009251	0.002674
...chris/ib/HEARTDATA/ms020.fdf	857	1.004	0.0005962	0.01737	0.01091	0.01048	0.003134

Figure 37. Statistics Output Generated by Print Stats Button

Data Output

Once the statistics have been output to the Info Messages window, there are several ways you can save the data in a file.

- Use standard cut-and-paste methods to select a part of the data and paste it into another document.
- Select the Messages/Info Messages/Save choice in the control panel to display the File Browser. This method allows you to save all of the current contents in a file.
- Press the *right* mouse button when the cursor is in the Info Messages text area, and select File/Save As, which opens the OpenWindows file browser.

Raw data values can also be dumped into a file. Selecting the Dump Data button writes the values of all the data pixels in all the selected ROIs into the file named in the File field. If the file name is not an absolute path, it is taken to be relative to the directory from which Image Browser was started. If the file name is blank, the data is written to the Info Messages window.

Currently, a hard copy of the histogram plot and the statistics graph can only be produced by capturing the screen output. OpenWindows has a utility program, Snapshot, that “takes a picture” of screen output; other documentation software, such as FrameMaker, have similar utilities.

Statistics from Multiple Images

To retrieve statistics from a specific location within an image over multiple images, perform the following steps:

1. Define the area to be analyzed by reading in an image and drawing an ROI around the desired area.
2. Save the ROI to a file.
3. Create enough Gframes to hold all the images.
4. If all the images are in one directory, read them all in using the Load All button.
5. Capture all of the Gframes by choosing Select All Frames.
6. Load the saved ROI, which is automatically drawn in all the selected Gframes that have images.
7. Update the statistics if the Statistics window is open, or select ROI Statistics if the window is closed.

This procedure generates statistics for the selected area in all the images, and is the sort of operation that could best be put into a macro.

Note that ROIs are fixed to the image as opposed to the screen. The Gframe can be made very large for positioning and drawing an ROI. When reading in images, Gframes can be made very small; the ROI is automatically positioned in the previously selected area of the image.

Image Rotation

Select the Image Rotation choice from the Process menu to open the small Rotation window, shown in Figure 38. The arrows on the buttons show how the images are transformed when the button is selected. The straight, double-headed arrows represent reflections of the image about an axis *perpendicular* to the arrow. The operation is applied to all selected frames.

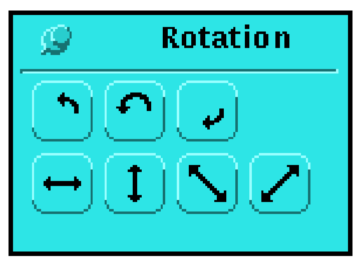


Figure 38. Rotation Panel

Note that the header information is also transformed on rotation or reflection, in order to keep track of the actual orientation and position of the slice in the magnet.

Image Arithmetic

Image Arithmetic is another processing function in Image Browser. Select the Image Arithmetic option from the Process menu in the control panel to open the Arithmetic window. This window allows addition, subtraction, multiplication, and division of two images or of an image and a scalar value.

The operands can be selected first, or the images can be selected first. Images are selected by selecting the Gframe where the image resides. The first Gframe is always selected with

the *left* button, and the following Gframes are selected with the *middle* button. The Operands field offers two options:

Image <op> Image	If this field is selected, two or three Gframes can be selected and the operation is executed according to the order given. If two Gframes are selected, the second one selected is also used to store the result. If three Gframes are selected, the third Gframe gets the result.
Image <op> Constant	If this choice is selected, a field for entering a constant is displayed in the Arithmetic window. One or two images can be selected and the operation is executed according to the order given. If one Gframe is selected, that one is also the result image. If two Gframes are selected, the second Gframe gets the result.

Filtering

Image Browser provides filtering. Select a filtering operation by choosing Image Filtering from the Process menu. When selected, a Filter window, as shown in Figure 39, opens.

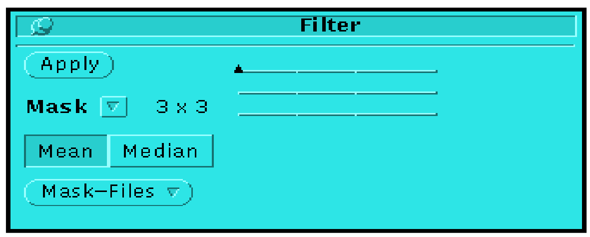


Figure 39. Filter Window

When Mean filtering is selected, as in Figure 40, each data pixel in the image is replaced by the average of the surrounding 3×3 or 5×5 squares of pixels, weighted according to the given filter mask. The 3×3 filter is the default size when the window first opens. The filter size is selectable using the *right* mouse button on the Mask field. Filter files can be saved and retrieved in the same manner that ROI files are saved and retrieved. The directory for Filter files is `$BROWSERDIR/filter`. Some example filters are provided, but personal filters can be easily created.

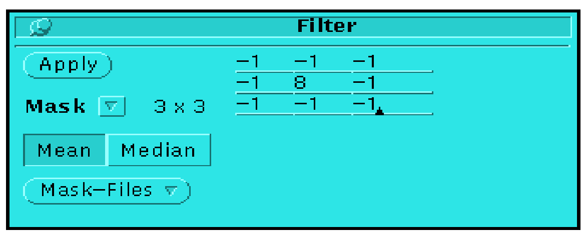


Figure 40. Filter Window with Data

When Median filtering is selected, only the size of the mask is significant. The weights are not used. Each data pixel value is replaced by the median data value in the surrounding 3×3 or 5×5 square.

A source Gframe with the image to filter must be selected before clicking on the Apply button to start the filter operation. Optionally, a second Gframe can be selected for the destination image. If only one Gframe is selected, the filtered image overwrites the source image.

Histogram Enhancement

Images can be enhanced using histogram methods. Select the Image Histogram Enhancement option from the Process menu to open a Histogram-Enhancement window, as shown in Figure 41.

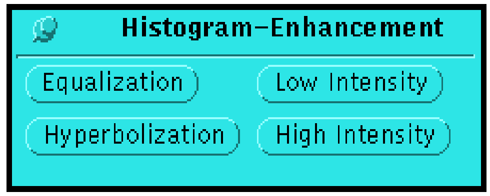


Figure 41. Histogram Window

The histogram function performs equalization, low-intensity enhancement, high-intensity enhancement, and hyperbolization. The function works by looking at a histogram of the intensities and enhancing the intensity histogram according to the selection.

Cursor and Line Functions

Click the *right* mouse button on Cursor Data in the Process menu to obtain cursor (distance and intensity) information. The popup window is blank until a point ROI is drawn.

Cursor Data

Cursor Data uses the point ROIs when obtaining information, and provides point intensities, coordinates, and the distance between the just selected or drawn point and the last selected point. The cursor function is most useful for searching for distances between slices in a multislice experiment or between slices in two different experiments, as long as the location information is present in the header of both images.

Figure 42 shows a Cursor Data window. Coordinates provide the absolute position of the cursor in the magnet reference frame.

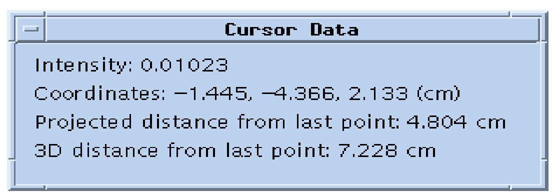


Figure 42. Cursor Data Window

The projected distance is only meaningful between slices with the same orientation and X-Y position. Distance is determined by drawing both pictures at the same scale and lining up the upper-left corners. The 3D distance is correct between any two images.

Line Data

Line Data uses line or polyline ROIs when obtaining information. The popup window is blank until an appropriate ROI is drawn or selected. The Line Data window provides coordinates, lengths, traces of intensities on the line, and projections of intensities across the line. Figure 43 shows a window with an intensity trace displayed.

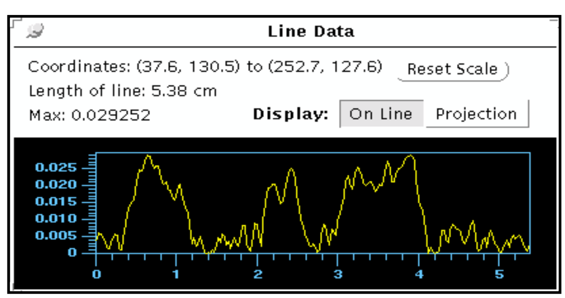


Figure 43. Line Data Window

On Line in the Display field displays a trace over the currently selected line ROI. Projection displays the maximum intensity projection across the line (the projection function is not available for polylines). The on-line plot is updated in real time as you move the line around, but the projection plot is not updated until you stop moving the line and release the *left* mouse button.

4.5 Macros

Image Browser incorporates the MAGICAL II macro programming language, which allows the definition of scripts, or macros, that perform a sequence of Image Browser commands. The MAGICAL language is described in detail in the manual *VNMR User Programming*; this section covers only those aspects of macro programming that are unique to Image Browser. The command syntax, conditional statements, and looping constructs, which give the language its basic flavor, are the same as in VNMR.

Note: The macro capability included in VNMR version 5.3 is a partial implementation. Many functions that should be callable from macros do not yet have macro commands, and the user interface is a simple prototype version.

User Interface

Click the Macro button to open the Macros window shown in Figure 44.

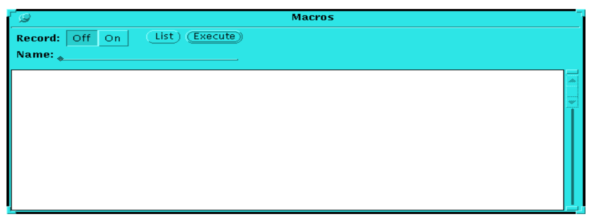


Figure 44. Macro Window

Name

The simplest way to use the Macro window is to type the name of the desired macro to be run in the Name field, then press Return. The named macro, which should be a built-in command or in the directory `$BROWSERDIR/macro`, is run.

It is also possible to type any one-line sequence of MAGICAL II commands or program constructs on Name and run it by pressing Return. Although not a very convenient way to enter macros, it can be very useful for quickly trying out a macro construction. Used this way, Name is essentially like the command line in VNMR.

Every time Return is pressed, the macro is run; it is not erased from the Name field.

Record

Record On/Off controls the automatic recording of macros. Record On records every user action (currently supported by a corresponding macro command) in the scrolling text window of the Macro panel. The recording is in a form that, when replayed, duplicates user actions. Macro commands can also be directly typed into the script.

Press the *right* mouse button in the scrolling window to display TextEdit options.

New user actions are always inserted at the current cursor position. Remember to move the cursor to the end of the text — below the last line — after doing any manual editing.

Before running the macro script created in the scrolling window, store it in your `macro` directory. To store the script, display the menu in the scrolling text window and select File/

Save As. The default save directory is the directory from which Image Browser was started, so manually create the directory `$BROWSERDIR/macro` before entering the file name. Once the script has been saved, run the macro by typing its name in the Name field, then press Return. (Of course, the macro can also be run from other macros just by using its name.)

List

The List button loads macro text specified in the Name field into the scrolling text window, obliterating any existing text. If the named macro does not exist, List does nothing; there is no error or warning message. If macro recording is on, make sure that the cursor is in the desired location after running List.

Execute

The Execute button is equivalent to pressing Return on the Name line. Note that the contents of the Name line, *not* the contents of the scrolling window, are executed.

Macro Capabilities

Parameters, operators and reserved words, and VNMR and Image Browser commands can be run as macros.

Parameters

Parameters are supported the same as in VNMR, as are multiple parameter trees and parameter groups. However, Image Browser makes no distinction between different trees and groups.

Operators and Reserved Words

Image Browser MAGICAL II has the same reserved words and operators as VNMR MAGICAL II, as listed in the manual *VNMR User Programming*, except that the two special operators `typeof` and `size` are not operational.

Built-in Commands

Most VNMR commands are inappropriate for Image Browser and are unavailable; many of these commands acquire and analyze NMR data. A small number of VNMR commands are of a more general nature.

The following VNMR commands are also available in Image Browser. Each command is used exactly the same as in VNMR; see the `format` listing regarding an extension.

Command	*Action*
`create`	Create new parameter in a parameter tree.
`destroy`	Destroy a parameter.
`destroygroup`	Destroy parameters of a group in a tree.
`echo`	Output from `echo` appears in Info Messages window and is searched for relative to $BROWSERDIR/roi directory.

Command	*Action*
`format`	Similar to VNMR `format` command, but with the following extension: `format(number,length,precision)` interprets a string length with a leading “0” to mean pad the output string to specified length with leading zeros, e.g, `format(17,'05',0):str` sets `str='00017'` `format(17,5,0):str` sets `str='17'`.
`groupcopy`	Copy parameters of a group from one tree to another.
`length`	Determine length of a string.
`rm`	Delete file.
`string`	Create a string variable.
`shell`	Similar to VNMR `shell` command, but at least one argument is required. Cannot be used to open an interactive shell window.
`substr`	Select a substring from a string.

Image Browser Commands Not In VNMR

The following Image Browser commands, by type, are not in VNMR.

General Commands

`tool`

Shows the Tools panel.

ROI Commands

`roi_bind('on','off')`

Turns on/off ROI binding.

`roi_delete`

Deletes all selected ROIs.

`roi_load(file)`

Loads an ROI stored in a named file into all selected Gframes. If `file` does not begin with a `/`, it is searched relative to the `$BROWSERDIR/roi` directory.

`roi_save(file)`

Saves all selected ROIs in a named file. If `file` does not begin with a `/`, it is presumed to be relative to the `$BROWSERDIR/roi` directory.

`zoom_factor`

Sets the factor by which zooming keyboard accelerators enlarge or reduce an image (see page 79).

Frame Commands

`frame_split(nrows,ncols)`

Splits all selected Gframes into number of rows and number of columns.

`frame_delete('selected'|'unselected'|'empty'|'all')`

Deletes Gframes of a specified type.

`frame_clear('selected'|'unselected'|'all')`

Clears (remove images from) Gframes of a specified type.

`frame_select('all'|'none'|n<,m ...>)`

Selects or deselects all Gframes, or selects specific Gframes by number. For example, `frame_select('none',1,2,3)` selects only frames 1, 2, and 3.

`frame_load(file)`

Loads Gframes in `file` into the graphics region.

`frame_save(file|fullpath)`

Saves selected Gframes in `file` into the graphics region. If a file does not begin with `/`, it is taken to be relative to the `$BROWSERDIR/gframe` directory.

Display and Intensity Commands

`display_vs_bind('on'|'off')`

Turns on/off V-scale "binding" property.

`display_vs(max)`

Rescales images in all selected Gframes so that the data value `max` is at the top of the intensity scale.

`display_vs(x,y<,nframe>)`

Rescales images. If `nframe` is not given, this command rescales images in all selected Gframes as if you clicked the V-scale tool at the data coordinate (x, y) in the image. If `nframe` is given, this command rescales only the image in the Gframe number `nframe`.

`display_contrast`

Shows Gamma Correction tool.

`display_contrast(slope)`

Sets display contrast to a specified slope with 50% gray in center of colormap ramp. `slope=1` corresponds to the default.

`display_contrast(min_intensity, max_intensity)`

Sets display contrast to a linear ramp with minimum and maximum intensities specified. Black is 0 and white is 1.

`display_contrast(min_intensity,max_intensity,gamma)`

Sets display contrast for gamma correction and linearity intensities steps with minimum and maximum intensities specified. Black is 0 and white is 1. `gamma` is the exponent in the relation $I = k \cdot V^{\gamma}$.

`display_contrast(min_intensity,max_intensity,gamma,contrast)`

Same as previous command; `contrast` is the ratio of maximum to minimum intensity displayable by a monitor.

`display_saturation('on'|'off')`

Turns on or off "Show Saturation" choice in Gamma Correction window.

Option Commands

`memory_warning_threshold(level)`

Sets a percentage threshold level for memory warnings. If more than `level` percent of system memory is in use, warnings might be generated when data is loaded. The default is 80%.

Data File Commands

`data_header_set('parname','command')`

Creates and sets new “float” type header variables in images already loaded into Image Browser. These values are NOT put into the image files on disk UNLESS you save the modified images.

This command creates the header parameter `parname` (if it does not exist) in all selected images, then sends the command line `command` to the UNIX shell. The standard input of `command` is a list of names of the selected images (in the order that the images were selected). The output should be a list of numbers, which are the values to assign to `parname` in the headers.

For example, if a file called `data` in the current directory contained a list of three numbers separated by spaces, tabs, or new lines, the following commands select frames 1, 2, and 3 and set the header parameter `myparm` in the three images to the respective values of the three numbers in the `data` file:

```
frame_select('none', 1,2,3)
data_header_set ('myparm','cat data')
```

`data_load`

Shows the File Browser window in Load Data mode.

`data_load(file)`

Loads an image in `file` into the next available frame. If `file` does not begin with `/`, it is taken to be relative to the current directory shown in the File Browser: Data window (see Figure 45). Loading an image with this command from a different directory does not change the current directory.

`data_load_all <(dir)>`

Loads all images in a directory. If you specify a directory from which data is to be loaded, it must be a full path. If you do not specify a directory, this command loads an image from the current directory as shown in the File Browser: Data window.

`data_save(file)`

Saves data in selected frame(s) in the named file. If more than one frame is selected, the name must include a wildcard character (see “Storing Images,” page 106). If `file` does not begin with `/`, it is taken to be relative to the directory shown in the File Browser:Data window.

3D Data Commands

`vol_extract (<'xy'|'yz'|'xz'>, first_slice [,last_slice <,incr>])`

Extracts one orientation of planes as selected by `'xy'` (the default), `'yz'`, or `'xz'`. Operates on the 3D data set to which the slice extractor is pointing (if you just loaded a 3D data set, it is that one). Specifying only `first_slice` extracts only that plane number. Specifying `last_slice` extracts planes from `first_slice` to `last_slice`. `incr` (the increment number between successive slices) must be positive if used.

`vol_mip (<'xy'|'yz'|'xz'>, first_slice [,last_slice <,incr>])`

Constructs an image, which is the pixel-by-pixel maximum of all the slices that `vol_extract` would have extracted. Arguments are the same as `vol_extract.`

Processing Commands

`info_save('filepath')` saves the contents of the Info Messages window to the file `'filepath'`. If `filepath` is not an absolute path, the contents are saved in the current directory in the File Browser Info Messages window. `filepath` also erases the current info window contents.

Sets the number of bins used for histogram in the Statistics panel to `n`.

`math('expr')`

Executes the expression '`expr'` in the same way as if it had been typed into the Image Math panel.

`stat_bins(n)`

Sets the number of bins used for histogram in the Statistics panel to `n`.

`stat_print`

Prints current statistics to the Info Messages window.

`stat_print('filepath')` or `stat_print('filepath','w')` writes the statistics directly to the file rather than to the Info Messages window. The format is similar to format used in the window except that the printed file is not truncated. This command deletes any previous contents of the file. If `filepath` is not an absolute path, the contents of the Info Messages window are saved in the directory that was open when Image Browser was started.

`stat_print('filepath','a')` is similar to `stat_print('filepath')` except that output is appended to the previous file contents.

`stat_update`

Updates statistics in the Statistics panel.

`stat_xcoord('roi'|'z'|'area'|'volume'|'integrated'|'mean'|`
`'median'|'min'|'max'|'sdv'|'$user')`

Sets the *x*-coordinate of statistics display for multiple ROIs.

`stat_ycoord('area'|'volume'|'integrated'|'mean'|'median'|`
`'min'|'max'|'sdv')`

Sets the *y*-coordinate of statistics display for multiple ROIs.

`rotate('90'|'180'|'270'| 'flip'|'flip0'|'flip45'|`
`'flip90'|'flip135')`

Rotates (or reflects) images in selected Gframes. The first three arguments rotate an image counterclockwise by specified amount in degrees. `flip` number arguments reflect an image through an axis perpendicular to a specified direction. A number specifies the direction of the corresponding double-headed arrow in the Rotation panel. The argument '`flip'` is equivalent to '`flip0'`.

Startup Macro

When Image Browser is first started, the macro `startup` is executed. This macro allows customizing some aspects of Image Browser’s operation.

4.6 Files and Other Items

This section describes file input and output, and the error and information displays.

File Browser

The File Browser is a standard interface used for storing and retrieving files. It is used when saving files and when retrieving image files.

The Gframe, ROI, and Filter interfaces use the File Browser for saving files, but they do not use it for retrieving files, because the Load interfaces are built for quick access and always assume a specified directory. For more information about the particular directory for these interfaces, see "Getting Started," page 68.

Figure 45 is an example of a File Browser window for loading images. The basic File Browser window is the same for most operations.

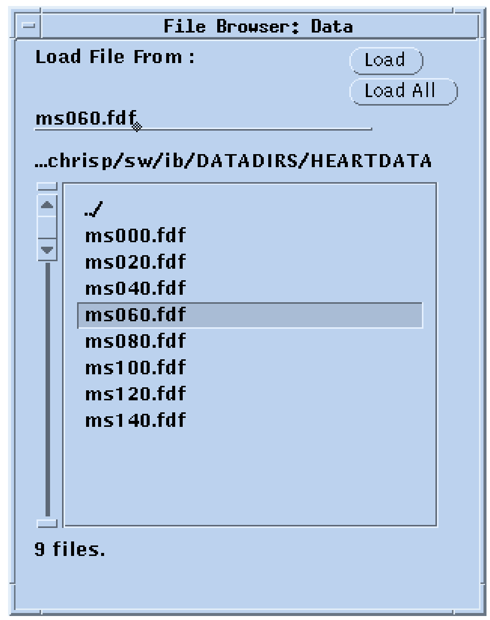


Figure 45. File Browser for Loading Images

The title of the window (in this case, File Browser: Data) describes the use of the current File Browser window. In the case of loading movie images, the title is Movie Frame Loader; for ROIs, it is File Browser: ROI. When files are saved, Load is replaced by Save. Load All does not change because there is no corresponding Save All command.

The File Browser window displays the currently selected file on the top line. Below that file is the current directory. The number of files in the directory is listed at the bottom. There is a scrolling window that contains the names of all the files in the directory. Subdirectories are indicated with a "/" at the end of their name. To select a name in the scrolling list, position the cursor over the desired name and click the *left* mouse button.

Changing Directories

To change directories, use the *left* mouse button to double click on the directory name. Select the name so it appears in the top line, then press the Return key. Changing directories can also be accomplished by entering the name directly in the top line and pressing Return. The UNIX prefix "~" works in File Browser. The "../" entry moves you to the parent directory.

Loading Files

Select the Load pulldown menu item from the File command panel item to open a File Browser window for loading files. To load a file into Image Browser, select the desired file and click on the Load button. Files are loaded into the next available graphics frame. To select a particular frame to load an image into, that frame should be selected immediately

before clicking the Load button. If there are no Gframes, a single Gframe is created that fills the entire graphics region and the image is loaded into it.

To load all the files in the current directory, click the Load All button.

Loading Images

Load FDF files by selecting the FDF file and clicking the Load button. For VNMR phasefiles, the directory that contains the phasefile must be selected when the Load button is clicked.

Loading 3D Images

Image Browser can load 3D data sets that are in FDF format. These are identified by having a "rank" of 3 and a "spatial_rank" (or "subrank") of "3dfov" specified in the header.

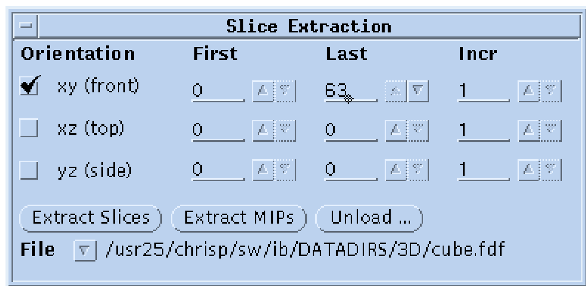


Figure 46. Slice Extraction Window

When a 3D data set is loaded into Image Browser, the Slice Extraction window shown in Figure 46 opens. This window has a File menu where the name of the current 3D data set is selected and displayed. To extract slices, first make sure that an appropriate Gframe is selected to load into. Also, make sure that the desired data set is selected in the File menu. Then, in the extractor window, check off the slice orientations desired and the range of slice numbers. The increment (Incr) may be set to some *n* greater than one to load only every "*n*th" slice. Press the Extract Slices button to actually load the selected slices. If there is only one Gframe, it will be split into enough frames to hold all the slices.

Maximum Intensity Projections (MIPs) can also be extracted by selecting the Extract MIPs button in the Slice Extraction window. This option extracts up to three MIPs, one for each orientation. A MIP slice is created by assigning each pixel in a MIP the highest intensity of that pixel in any of the slices that would be extracted by the Extract Slices button.

To delete a data set from Image Browser memory, select the data set in the File menu and press Unload (however, the file will not be deleted from the disk).

The separate program `disp3d` can be used to look at a 3D data set more directly and determine which slices are of interest. See the manual *VNMR Command and Parameter Reference* for more information on `disp3d`.

If the Slice Extraction tool has been closed, it can be opened again by selecting Slice Extractor from the Tools button menu.

Saving Files

Select the Save menu item from the File option on the control panel to open a File Browser for saving files.

To save an image, a graphics frame, a ROI, or a filter to a file, make sure the desired item is selected, then type or select an (existing) file name into the top line and click the Save button. That item is saved in the current directory under the file name given.

Storing Images

If more than one frame is selected, all the images are written out, and one of two possible wildcards must be used in the file name. Wildcards permit the basic name to be specified, while allowing the program to fill in a specified field for each file. The * wildcard specifies the "base" name of the image, everything up to the final ".x" extension. For example, if the image is read from the file `bee.knee0013.fdf`, specifying `*.jpg` puts the output in the file `bee.knee0013.jpg`. The # wildcard specifies the first numeric field in the image's file name. In the previous example, specifying `my_knee_#` writes the data to the file `my_knee_0013`.

It is also possible to use the # wildcard if there is no numeric field in the image's file name (i.e., no digits). In such a case, the `save_` command automatically assigns index numbers to the output images. This feature is especially useful for saving slices that have been extracted from a 3D data set, because then all the slices have the same name (the name of the original data set). For example, if slices are extracted from the 3D data set `heart.fdf`, specifying either `heart#fdf` or `*#.fdf` assigns the slices the names `heart0001.fdf`, `heart0002.fdf`, etc.

By default, all data are stored in floating point FDF format. Other formats can be selected from the File menu selection list. Position the cursor on the File menu option, press the *right* mouse button, and then select Output Format. The Output File Format window opens. The basic format is selected by pressing the *right* mouse button on the Format Type field. Besides FDF, Table 7 lists the other available formats.

The data type in the output file ("Integer" or "Float") as well as the data size (8, 16, or 32 bits) is purportedly set independently. However, almost all of the types support only 8-bit integer data, and all except FITS and FDF are converted to 8-bit integers during the dumping process.

For all integer formats, the data is scaled to match the currently displayed "Vertical Scale" of the image. That is, pixels that are saturated (set to the maximum value) in the current display are set to the maximum integer value in the output file, and other pixels are scaled proportionally. For scaling to properly work, the data type in the Output File Format window must be set to integer; otherwise, the data is scaled to map the brightest pixel to the maximum integer value. (This problem is caused by the `convert` routine when a floating point FITS file is converted to an integer format.)

The available formats are specified in the file `$BROWSERDIR/fileformats.init`. This file lists the format names and specifies a shell command that converts a FITS file into that format. If a non-FDF format is selected, Image Browser dumps the data in the FITS format, and then calls another program to convert it to the requested format. All the supplied formats use the `convert` program from the ImageMagick display package; see "ImageMagick Package," page 107 to do the conversion. `convert` always produces an 8-bit precision (maximum) output file, even if the format supports more bits and they are present in the input.

To add new formats, obtain a program that converts from the FITS format (or any supported format) to the desired format; see the section "Flexible Image Transport System." Then add lines to the `$BROWERDIR/fileformats.init` file, and specify the new name and the conversion script. The following example entry produces JPEG files:

```
format JPEG compressed format
script     convert -quality 85 fits:$1 jpeg:$2
data       integer 8
```

The label `JPEG` appears in the popup menu of format types; the comment on the remainder of the format line is ignored. The conversion script is everything on the line after the script

Table 7. Formats Available in Image Browser

Format	*Description*
AVS	AVS X image file
BMP	Microsoft Windows bitmap image file
EPS	Adobe Encapsulated PostScript file
FAX	Group 3 FAX
FITS	Flexible Image Transport System
GIF	Compuserve Graphics Interchange Format (version 89a)
GIF87	Compuserve Graphics Interchange Format (version 87a)
JPEG	Compressed format from Joint Photographic Experts Group
MIFF	Magick image file format
PCD	Photo CD
PCX	ZSoft IBM PC Paintbrush file
PDF	Portable Document Format
PICT	Apple Macintosh QuickDraw/PICT file
PGM	Portable gray map
PNG	Portable Network Graphics
PS	Adobe PostScript file
PS2	Adobe Level 2 PostScript file
SGI	Irix RGB image file
SUN	Sun Rasterfile
TGA	Truevision Targa image file
TIFF	Tagged Image File Format
VIFF	Khoros Visualization image file
XBM	X11 bitmap file
XPM	X11 pixmap file
XWD	X Window System window dump image file

label. Conversion scripts are currently limited to one line of, at most, 1000 characters. Before the script is run, the symbol `$1` is expanded into the name of a FITS format input file containing the data. The output file name is represented by `$2`. In this case the script includes a "quality" flag that controls the amount of data compression to be done. The data line specifies the type and size of data that JPEG supports, but it is currently ignored.

One limitation of dumping files in a non-FDF format is that the aspect ratio of the image is not preserved. Image Browser dumps out the actual data, rather than an image of it. Most image formats assume that the individual pixels are square and do not have *x* and *y* scaling information in their headers. The FITS format does have such information in its header and it is filled in appropriately by Image Browser, but `convert` ignores it, and most viewers ignore it when they display the FITS file.

ImageMagick Package

The ImageMagick package is free by anonymous FTP from various Internet sites such as `ftp.x.org` in the directory `contrib/applications/ImageMagick`. Also, see `www.wizards.dupont.com` for precompiled binaries.

Flexible Image Transport System

The Flexible Image Transport System (FITS) file format specification is available by anonymous FTP from `fits.cv.nrao.edu` in the directory `fits/documents/standards`. FITS was selected as the standard format because it is a true data format rather than just an image format. It supports integer and floating point data and has header entries to specify the original image scale and aspect ratio. More information is available at `www.gsfc.nasa.gov/astro/fits/fits_home.html`.

Redisplaying Graphics Frames

The Refresh option on the control panel refreshes and redisplays all graphics frames.

Displaying Error and Info Messages

The Messages pulldown menu on the control panel contains the options Error Messages and Info Messages.

Error Messages

The Error Messages option opens an Error Messages text window. This window is scrollable so that all previous error messages can be viewed. If there is an error, the Error Message window automatically opens on the screen. The window can stay on the screen or be closed. Error messages can be saved into a file or all messages can be deleted.

Info Messages

The Info Messages option opens an Info Messages text window. This window is scrollable so that all previous info messages can be viewed. The Info Messages window is for output of information from a particular task, such as statistics. The window automatically opens when statistics or other information is output to it. The desired information can be then be selected and output to a file, and the messages can be deleted. The window can be closed or moved to a different location.

Reading VNMR Image Files

The VNMR data that can be read are not files but directories, which must contain a `phasefile` and a `procpar` file. Currently, the directories are either the current experiment directory or the directories saved with the command `svdat`. To read a VNMR image, use File Browser to select the directory that contains the `phasefile` file and the parameter file, then select the Load button in File Browser. To read experiment images, the `exp1`, `exp2`, ..., or `exp9` directory must be selected.

Working with FDF Files

The Flexible Data Format (FDF) file consists of a header and data:

- The header is an ASCII header, and its fields are defined by a DDL (Data Definition Language). Having a ASCII header makes it easy to decipher the image content and add new fields. Also, the format of the header is the same as the ASCII format of the `procpar` file.
- The data portion is binary data described by the header fields. It is separated from the header by a null character.

For a definition of all the fields, see the section *FDF File Specification* in the manual *VNMR User Programming*.

Creating FDF files

FDF files can be generated by VNMR from FID files produced by standard SISCO imaging sequences using the `svib` or `svsis` macro. `svsis` can be modified for special user-defined sequences. If standard SISCO parameters have been used, the modification can be as simple as adding a line to define the sequence. The `svib` and `svsis` macros are described in the manual *VNMR Command and Parameter Reference*. For 3D images, the `ft3d` macro can produce FDF files.

Another way to create FDF files is to edit or create a header defining a set of data with no headers and attach it to the data file using `fdfgluer`, which has the syntax:

```
fdfgluer header_file <data_file <output_file>>
```

This UNIX executable takes a `header_file` and a `data_file` and joins them to form an FDF file. It also calculates a checksum and inserts it into the header. If there is no `data_file` argument, `fdfgluer` assumes the data is input from the standard input, and if there is no `output_file`, it puts the FDF file to the standard output.

Splitting FDF files

The UNIX command `fdfsplit` takes an FDF file and splits it into its data and header parts. The syntax is `fdfsplit fdf_file data_file header_file`.

The header can still have a checksum value in it, which should be removed.

Chapter 5. Image Browser Math Processing

Sections in this chapter:

Image Browser Math is used in conjunction with the Math Tool described previously in Chapter 4, “Image Browser,” Image Browser Math provides a way to do more complex processing than “image arithmetic,” but requires more processing overhead. Instead of being limited to simple four-function operations, any function that can be expressed in the C language can be specified.

Operations in Image Browser Math are defined as either expressions or functions:

- *Expressions* are specified by typing any legal C expression into the Image Browser Math Panel, using symbols such as `#5` to specify images. The expression is applied to each data pixel, and each output data pixel value is a function of the values of the corresponding data pixels in the input images. Operations can involve an arbitrary number of input images, as well as the X and Y coordinates of the data pixel within the image.
- *Functions* are used for operations that cannot be specified in a single expression. You write a C subroutine that performs the desired operations.

5.1 Opening Image Browser Math

Image Browser Math works on either 2D or 3D data sets. For operations with expressions the image operands must all be the same size. The following steps open the program:

1. Select the Image Browser Math choice from the Process menu in the Image Browser control panel. The Image Math window shown in Figure 47 is displayed.

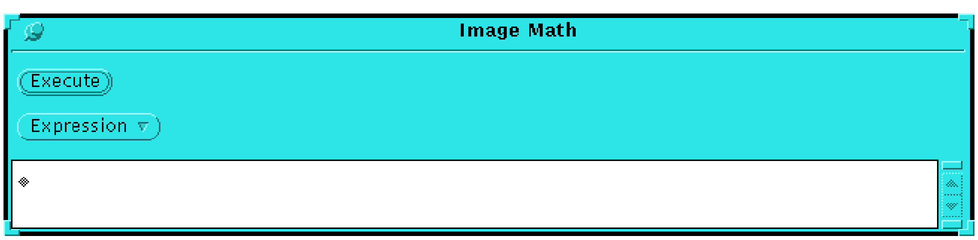


Figure 47. Image Browser Math Panel

2. Type an expression or function into the scrolling window at the bottom of the panel.

   You can use the Expression button to automatically enter a previously compiled expression.

3. For either expressions or functions, you need to specify which images are to be operated on. Images are specified by their graphic frame (Gframe) numbers, using symbols such as `#n`, in which `n` is the number of a Gframe containing an image.

   To automatically enter Gframe numbers, do the following procedure:

   a. Select the Image Browser Math process.
   b. Click the mouse cursor inside a Gframe.

      The number of that frame is entered in the Image Browser Math equation area at the current cursor location. If the cursor is positioned just after a #, only the Gframe number is entered, and any preexisting number is deleted; otherwise, a # and the Gframe number are inserted.

5.2 Image Browser Math Expressions

Legal expressions are in the form of standard C expressions, with the image specifiers, `#n`, treated like “float” type C variables in evaluating the expression. For example, the following expression calculates the average of the images in Gframes 1, 2, and 3 and puts the result in Gframe number 4:

```
#4=(#1+#2+#3)/3
```

After typing the expression, you must click on the **Execute** button to carry out the operation. The expression is evaluated for each data pixel to calculate the output image.

The first time an expression is entered and executed, it is edited and inserted into a C program, which is then compiled and stored in the directory `$BROWSERDIR/math/expressions/bin` as a dynamically loadable library. This library is then linked to the running Image Browser program, and the input images are passed to the routine containing the user’s new expression. This routine calculates the output image and then returns to the main Image Browser, which loads it into the appropriate Gframe. Finally, the library is unloaded. If the same expression is used a second time, possibly with different image numbers, the compilation step is skipped in the above sequence, because the precompiled program can be used.

Precompiled expressions are stored in `$BROWSERDIR/math/expressions/bin`. A list of these programs is available in the Expression menu. Each choice is the right side of a precompiled equation, with the Gframe numbers (but not the #s) and any spaces removed. When an expression is selected, it replaces whatever is in the window, prefaced with #=, and the cursor is placed after the first #. The Tools panel is also put into Math mode. To use a precompiled expression, do the following steps:

1. Select the desired expression from the Expression menu.
2. Click on the Gframe where you want the result to appear. The number is inserted and the cursor advances to the next #.
3. Click on source images until all the image numbers are filled in.
4. Click on Execute.

Variables Used in Image Browser Math Expressions

Certain variables can be used in an expression. Variables `i`, `j`, and `k` respectively contain the column, row, and plane of the current data pixel, as shown in this example:

```
#3 = abs(i-j)<30? #1 : #2
```

This expression copies a 60 pixel wide diagonal band of image #1 into Gframe #3 and sets the rest to image #2. An expression should not modify `i`, `j`, or `k`.

Note that the C construct "*expression0? expression1:expression2*" is a compound expression that returns the value of *expression1* if *expression0* is true (or nonzero) and the value of *expression2* otherwise.

The variables width, height, and depth contain the number of columns and rows in the image. For example, the following expression copies image #1 to Gframe #2, leaving a 6-pixel-wide border of zeros around the edge:

```
#2=i>5&&i<width-6&&j>5&&j<height-6?#1:0
```

An expression should not modify width, height, or depth.

These `i`, `j`, `k`–width, height, and depth–variables appear to make it possible to construct a synthetic image without any input image. However, some input image is required in order to establish image parameters such as width and height, as well as everything else that is in the file header, for example:

```
#2=(#1,exp(-((width/2-i)*(width/2-i)+(height/2-j)*
     (height/2-j))/2500.0))
```

This expression creates a Gaussian spot in the middle of the image that is 100 data pixels wide. The output image has the same shape and size as image #1. Note that the denominator 2500 is written in floating point (2500.0) so that the division does not give truncation errors and that the `exp()` function gets a float type argument, as it expects.

The C construct "*var=(expression1,expression2)*" is used in the previous example. Expressions in parentheses are evaluated left to right and only the value of the last expression is kept. So, in this case, *var* is set equal to the value of *expression2*. In this example, the value *expression1* is only a dummy to give the program information about the image format, but it could affect the final value; for example, `var=(x=2,x+3)` sets `var` equal to `5` and `x` equal to `2`.

Finally, there are variables available for temporary storage that are not preassigned any values. The variables `x`, `y`, `z`, and `r[0]` through `r[99]` are available for you to store floating point values. The variables `ii`, `jj`, `kk`, and `n[0]` through `n[99]` are integer variables. These variables can be used for efficiency, to avoid recalculating complicated expressions, as in the following example:

```
##2=(#1, x=width/2-i, y=height/2-j, exp(-(x*x+y*y)/2500))
```

Note that in this example, unlike the previous example, 2500 is written as an integer, because temporary variables `x` and `y` are floats that force the division to be done in floating point. Using temporary variables like this often makes expressions more readable.

5.3 Image Browser Math Functions

Sometimes you might need to perform an operation that cannot be put into a single C expression; such cases require user functions. An Image Browser Math function is distinguished from an expression simply by whether the first field to the right of the equals sign is the name of an existing function. The following example shows how user function `foo` is activated:

```
#11 = foo ##1-8 "bar" 7
```

Here, the expression calls `foo`; passes it images 1 through 8, the string `bar`, and the number `7` as input; and puts the output of `foo` in frame 11.

Image Browser Math Function specifications are not parsed as C expressions, so the syntax format is not strictly defined. However, for the sake of consistency, and to be compatible with future versions, use the style in the last example. Note that double quotation marks s are required around every string argument to be passed.

Specifying Images in Functions

Image Browser Math Functions allow lists, or "vectors," of images to be specified. The following form is the most general form for specifying an image vector:

```
#(image_list)
```

`image_list` is a list of frame numbers separated by commas, and optionally including ranges of frame numbers denoted by hyphens. For example, the statement

```
#11 = maxof #(1,3,8-10,6)
```

returns the maximum of images 1, 3, 8, 9, 10, and 6.

The simple `#3` notation, as used in Image Browser Math Expressions, specifies a vector with one element, and is equivalent to `#(3)`. If the vector only contains one range of consecutive frame numbers, it can be abbreviated as `##1-10`.

Be aware that a construction like `#1 #3 #8 #9 #10 #6` does *not* specify a vector of images but rather six vectors, each containing one image. Some programs, such as `maxof`, can treat the two cases identically, but others, such as `fit` discussed on page 120, do not.

Image Browser Math Functions can also produce more than one output image. In such cases, the output images must be specified as an image vector:

```
##11-12 = maxof ##1-10
```

In this example, `maxof` writes the maximum intensity image to frame 11 and writes a map of which image had the maximum intensity for each pixel in frame 12. Note that the following construction produces only one output image; the `#12` frame is ignored:

```
#11 #12 = maxof ##1-10
```

In summary, a vector of images can be specified three ways:

- `#1` specifies a vector with one element.
- `#1-10` specifies a vector with a single range of image numbers.
- `#(1-10,21,31)` specifies a vector with an arbitrary list of images.

Defining an Image Browser Math Function

Defining the `maxof` function involves defining a function called `mathfunc` in a file named `maxof.c`. (The process is similar to defining a user pulse sequence by defining the `pulsesequence` function in a file named after the sequence.) Function files are kept in the directory `$BROWSERDIR/math/functions/src`. The following procedure is an example of how you would define the file `maxof.c` in that directory.

File Header

First, enter the following line at the beginning of the file:

```
#include header "imagemath.h"
```

imagemath.h declares the global variables and functions needed to access the input and output images (imagemath.h also includes the most commonly needed standard UNIX headers, including math.h).

mathfunc Definition

Next, define the mathfunc function. mathfunc first checks to see if the input being passed is valid. If the input is not valid, mathfunc returns a FALSE value to the caller (if the function encounters no errors, mathfunc should return TRUE). Be aware that nbr_infiles and input_sizes_differ are global variables declared in imagemath.h and get set before the mathfunc() subroutine is called.

The maxof math function also calls the want_output() routine to ensure that there is someplace to put the first output image; want_output(n) returns TRUE if you have asked for the nth output image.

Image Dimensions

If the input images are all the same size (input_sizes_differ is FALSE), their common dimensions are in the global variables img_width, img_height, and img_depth, and the product of the three variables is in img_size. Some functions can deal with input images of different sizes. In such cases, you must use the arrays in_width[], in_height[], in_depth[], and in_size[]. These arrays determine the width, height, depth, and size for each individual image (unless otherwise mentioned, all arrays start indexing from 0, in typical C fashion).

Memory Allocation

The create_output_files() function allocates memory for all the requested outputs, making them all the same size as the input files. maxof limits the number of output files to two, and gives files header characteristics like those of the first input image.

Pixel Looping

The maxof function then loops over all the pixels in the input images:

- img_size has the number of pixels per input image.
- nbr_infiles has the number of images.

  The nbr_infiles variable has the total number of images in all input image vectors. To access individual image vectors, use the variable nbr_image_vecs, which provides the number of image vectors, and the array in_vec_len[], which provides the number of images in each vector.
- in_data[j][i] has the ith pixel in the jth input image.

  The maximum value in the ith pixel is written to the first output image, addressed as out_data[0][i]. If you were defining mathfunc, you have already checked the desired output number 0 at the beginning of the routine. At this stage, you must determine if output number 1 is desired. If it is desired, write the index of the image with the maximum value in output image number one.
- IN_DATA(i,j,k) references the kth pixel of the jth image in the ith vector.

Creating a New Function

Creating and compiling a new Image Browser Math Function is currently done manually. To create a function, perform the following procedure:

1. Create a file that defines the function mathfunc (e.g., myfunc.c. This file must reside in the $BROWSERDIR/math/functions/src directory.

2. Edit the `makemathfunc` file to add `myfunc.c` to the list of source files. The `make` macro variable `USRSRC` is a list of the source files for simple user programs, those that only involve one source file. Add the new file to the list by typing the following statement:

   `USRSRC = maxof.c myfunc.c`

   If the list increases to more than a single line, continue on the next line by putting a backslash (\) as the last character on the line.

3. After editing the `makemathfunc` file, enter the following command:

   `make depend`

   This command updates the list of files that the program depends on and changes the `makemathfunc` file (a warning `fit.c includes userfit.c more than once!` appears, which is normal.). Enter **`make depend`** only after you change `#include` directives in a file or change the `makefile` itself.

4. Enter **`make myfunc`** to compile the `myfunc` routine.

Variables, Macros, and Functions Available to User Functions

This section lists global variables, macros, and functions for use in `mathfunc` routines.

Global Variables

Except where noted, global variables are initialized before `mathfunc` is called.

`int nbr_image_vecs`	Number of image vectors passed to the user's program.
`int in_vec_len[]`	Array of length `nbr_image_vecs` giving the number of images in each input image vector.
`int vecindx[]`	Array of length `nbr_image_vecs` giving the index in the `in_object[]` and `in_data[]` arrays of the first member of each image vector. The rest of the members of a given vector sequentially follow in those arrays.
`int nbr_infiles`	Number of input images in all the image vectors put together.
`int input_sizes_differ`	Set to TRUE if the input images are not all identical in size. If the images are all the same size, it is set to FALSE.
`int img_width, img_height, img_depth,img_size`	If all input images are identical in size, these arrays have their dimensions. The `img_size` is the total number of data pixels.
`int in_width[], in_height[], in_depth[],in_size[]`	If input images vary in size, use these arrays to get the sizes of the individual images. The dimension of these arrays is `nbr_infiles`.
`FDFptr in_object[]`	Array of dimension `nbr_infiles` containing pointers to all the input image structures, and which can be treated either as a single array, containing every input image in every image vector, or as several arrays placed "end-to-end," one for each image vector. The starting index of each vector in the whole array is given in `vecindx[]`.
`float *in_data[]`	Array of dimension `nbr_infiles` containing pointers to all the input data arrays, and which can be treated either as a single array, containing every input image in every image vector, or as several arrays placed "end-to-end," one for each image vector. The starting index of each vector in the whole array is given in `vecindx[]`.

`int pixel_indx`	Used in the `fit` program to indicate which pixel is currently being `fit`. It can be referenced by the user's FUNCTION, JACOBIAN, or GUESS routines.
`int nbr_strings`	Number of strings passed to the user's function.
`char *in_strings[]`	Array of dimension `nbr_strings` containing pointers to all the strings passed to the user's function.
`int nbr_params`	Number of numerical constants passed to the user's function. In the `fit` program, this is modified in `fit.c` so that it does not reflect any threshold value that might have been passed.
`float in_params[]`	Array of dimension `nbr_strings` containing all the numerical values passed to the user's function. In the `fit` program, this variable is modified in `fit.c` so that it does not reflect any threshold value that might have been passed.
`int nbr_outfiles`	Number of output files that caller has requested from user function. In the `fit` program, this variable can be adjusted downward if more output files are requested than `fit` knows how to supply.
`int out_width[], out_height[], out_depth[], out_size[]`	Arrays of dimension `nbr_outfiles` that have the size of each output image. These arrays are initialized to match the size of the last input image, but you can adjust them before calling `create_output_files()`.
`FDFptr out_object[]`	Array of dimension `nbr_outfiles` containing pointers to all of the output image structures. It is initialized by `create_output_files()`.
`float *out_data[]`	Array of dimension `nbr_outfiles` containing pointers to all of the output image data arrays. It is initialized by `create_output_files()`.

Macros

`IN_DATA(vec,img,pixel)`	References pixel number `pixel` in image number `img` in input image vector number `vec`.
`TRI_ELEM(matrix,row,col)`	(In `fit` routines only). If `matrix` stores the lower triangle of a symmetric matrix, references the matrix element in row `row` and column `col`. Requires `row >= col`.

Functions

`FDFptr clone_ddl`	Makes an identical copy of the image structure `old_ddl`. If `dataflag` is FALSE, only the header values are copied, otherwise the data are also copied. Example: `FDFptr clone_ddl (FDFptr old_ddl, int dataflag)`

`FDFptr create_ddl`	Creates an image data structure of the given width, height, and depth, and returns a pointer to the structure. Example:
	`FDFptr create_ddl(int width,  \`
	`   int height,int depth)`

`int create_output_files`	Creates up to `n` output `files` (actually, just data structures in memory). File sizes are given by `out_width[]`, `out_height[]`, `out_depth[]` arrays. This function loads `out_object[]` and `out_data[]` with pointers to the data structures and data arrays, respectively. Example: `int create_output_files (int n, FDFptr cloner)`
`void *getmem`	Equivalent to system `malloc()` function, except that any memory allocated this way is freed when the user function is done. Example: `void *getmem (size_t size)` ***CAUTION:*** **Do not use `free()` to release memory allocated by `getmem()`.**
`int want_output`	Returns TRUE if output image number `n` is requested. If three images are specified for output in the Image Browser Math command line, `want_output(n)` returns TRUE if `0<=n<=2`; otherwise, this function returns FALSE. Example: `int want_output(int n)`

`get_header_int`	Gets the value of an integer-type header variable. The variable `name` is read from the image referred to by `handle`. The value of the variable is put into the integer pointed to by `pvalue`. Returns a logically true (nonzero) value on success, and a logically false (zero) value on failure. Example:
	`int get_header_int(handle,  \`
	`   name,pvalue)`
	`FDFptr *handle;`
	`char *name;`
	`int *pvalue;`

`get_header_double`	Gets the value of an double-type header variable. The variable `name` is read from the image referred to by `handle`. The value of the variable is put into the location pointed to by `pvalue`. Returns a logically true (nonzero) value on success, and a logically false (zero) value on failure. Example:
	`int get_header_double(handle, \`
	`   name,pvalue)`
	`FDFptr *handle;`
	`char *name;`
	`double *pvalue;`

`get_header_string`	Gets the value of an character-array-type header variable. The variable `name` is read from the image referred to by `handle`. A pointer to the character string is put into the location pointed to by `pstring`. Returns a logically true (nonzero) value on success, and a logically false (zero) value on failure. Example:
	`int get_header_string(handle,  \`
	`   name,pstring)`
	`FDFptr *handle;`
	`char *name;`
	`char **pstring;`

`get_header_array_int`

Gets the value of one element of an integer-array type header variable. The `index` member of the variable `name` is read from the image referred to by `handle`. The value of the element is put into the location pointed to by `pvalue`. Returns a logically true (nonzero) value on success, and a logically false (zero) value on failure. Example:

```
int get_header_array_int  \
(handle,name,index,pvalue)
FDFptr *handle;
char *name;
int index;
int *pvalue;
```

`get_header_array_double`

Gets the value of one element of a header variable that is an array of doubles. The `index` member of the variable `name` is read from the image referred to by `handle`. The value of the element is put into the location pointed to by `pvalue`. Returns a logically true (nonzero) value on success, and a logically false (zero) value on failure. Example:

```
int get_header_array_double  \
   (handle,name,index,pvalue) FDFptr
*handle;
char *name;
int index;
double *pvalue;
```

`get_header_array_string`

Gets the value of one string from a header variable that is an array of strings. The `index` string from the variable `name` is read from the image referred to by `handle`. A pointer to the character string is put into the location pointed to by `pstring`. Returns a logically true (nonzero) value on success, and a logically false (zero) value on failure. Example:

```
int get_header_array_string  \
   (handle,name,index,pvalue)
FDFptr *handle;
char *name;
int index;
char **pstring;
```

`get_image_width`

Returns the number of pixels in the *fast* image dimension. Example:

```
int get_image_width(handle)
FDFptr *handle;
```

`get_image_height`

Returns the number of pixels in the *medium* image dimension. Example:

```
int get_image_height(handle)
FDFptr *handle;
```

`get_image_depth`

Returns the number of pixels in the *slow* image dimension. Example:

```
int get_image_depth(handle)
FDFptr *handle;
```

`get_object_width`

Returns the width of the region imaged, in centimeters. Example:

```
double get_object_width(handle)
FDFptr *handle;
```

`get_object_height`	Returns the height, in cm, of the region imaged. Example:
	`double get_object_height(handle)`
	`FDFptr *handle;`

`get_object_depth`	Returns the depth of the region imaged, in centimeters. Example:
	`double get_object_depth(handle)`
	`FDFptr *handle;`

`get_dll_data`	Returns a pointer to the array of floats that represent the image. Example:
	`float *get_ddl_data(handle)`
	`FDFptr *handle;`

5.4 The Fit Program

The `fit` program is provided as a general-purpose routine to fit a function to a series of images. Output is one or more images that give the parameter value as a function of pixel location. You can also add new functional forms to be fit, as described in "Adding New Functional Forms," page 122.

For example, to run the `fit` program on t1 data, type the following statement in the Image Browser Math window:

```
##11-17 = fit ##1-8 "t1" "ti" .01
```

Look at the first two fields:

- `##11-17` specifies the *number of output images*, in this case, seven. These images contain, respectively, the three parameters of the fits, the RMS residuals, and the formal sigmas of the parameters. You can save on calculation time by asking for fewer output images. In this example, images that you do not ask for are not calculated. In practice, residuals take negligible time to calculate, and parameter sigmas increase the calculation time by less than a factor of two.
- The first field to the right of the equal sign (=), in this case, `fit`, is the *name of the program to run*. Since `fit` exists in `$BROWSERDIR/math/functions/bin`, Image Browser does not try to parse the name as an Image Browser Math Expression.

The remaining fields are passed to the `fit` program:

- `##1-8` is the *list of input images*.
- `t1` is the *type of fit* required. (`t1` does *not* need to be the first string parameter. Rather, the first string that names a known fit type is taken as the fit type specification.)
- `ti` is the *independent variable of the fit*, whose value is found in the header of the input images. Often, the desired independent variable values are put in the header when the image files are created (with `svib`), because any arrayed parameters will have their values put in. Otherwise, new header values can be set with the `data_header_set` command described on page 102. If the header parameter name happens to be the same as the fit type, enter the same string twice.
- Parameter `.01` is the *threshold value*. Pixels that have values in all the images with absolute value less than the threshold return zeroes in the output images. The default is 0.

Other string arguments can be entered on the command line:

- The string `quick` can be used to force nonlinear fits to bypass the iterative fitting procedure and use the initial guess for the parameter values as the final result. Depending on the accuracy of the initial guess function, this result might be useless, or

nearly as good as the results of the nonlinear fitting procedure. `quick` is also useful for checking the accuracy of a guessing function.

- The string `noderiv` directs the nonlinear fitting routine not to use derivatives of the fitting function with respect to the parameters that might be provided. In this case, the fitting routines will estimate derivatives numerically from finite differences. This option is mainly useful for testing.
- The strings `prev` or `noprev` are used to force the `USE_PREVIOUS_PARAMETERS` flag on or off. Be aware that `prev` breaks the `abst1` and `absqt1` routines, because their guess routines modify the data `prev`.

Types of Fits

As shown in the Table 8, the types of fits available are `t1`, `qt1`, `abst1`, `absqt1`, `t2`, `adc`, and `shames2`:

Table 8. Fit Types

		Fit Parameters		
Name	*Functional Form*	*P0*	*P1*	*P2*
t1	y=(M(0)-M_o)*exp(-t/T1)+M_o	T1	M(0)	M_o
qt1	y=A*(1-2*Q*exp(-t/T1))	T1	A	Q
abst1	y=|(M(0)-M_o)*exp(-t/T1)+M_o|	T1	M(0)	M_o
absqt1	y=|A*(1-2*Q*exp(-t/T1))|	T1	A	Q
t2	y=M(0)*exp(-t/T2)	T2	M(0)	
adc	y=M_o*exp(-b*ADC)	ADC	M_o	
shames2	y=BV*SBV_o*exp(-t*alpha)+PS*SBV_o*(1-exp(-t*alpha))/(alpha*(1-hct))	BV	PS	

- `t1` and `qt1` are alternative formulations for three parameter fits to T_1 data.
- `abst1` and `absqt1` are alternative formulations for three parameter fits to absolute value T_1 data.
- `t2` is a standard two-parameter fit to T_2 data.
- `adc` is a two-parameter fit to diffusion weighted images. The fitted parameters are the Apparent Diffusion Coefficient and the reference level.
- `shames2` is a two-parameter fit for image enhancement by a contrast agent as a function of time. The fitted parameters are for blood volume and permeability. There are three "fixed parameters" that can be set from the command line: `alpha`, `SBV0`, and `hct`. The following command is an example:

  ```
  #11=fit ##1-8 "shames2" "x" 0.01 0.136 0.13 0.37
  ```

  In this command line, the first constant (`0.01`) is interpreted as the *threshold level*; any pixels with an absolute intensity less than this value are not fit, but given zero values in the output images. This first constant is read by the basic fitting routine; any further constants can be read by the user function.

  The next example sets the following parameter values:

  ```
  alpha=0.136
  SBV0=0.13
  hct=0.37
  ```

  These parameters are also the default values.

You can also pass additional images on the command line. The first "extra" image is used as a baseline reference; its pixel value is subtracted from all the normal input images. The following command is an example.

```
#11=fit ##1-8 #9 "shames2" "x"
```

Here, the fit routine uses `#9` as the *reference image*. Up to three more additional images can be specified to set pixel dependent values of `alpha`, `SBV0`, and `hct`; these values override any "constant" values specified on the command line, such as:

```
#11=fit ##1-8 #9 #10 "shames2" "x"
```

Now, the fit routine sets `alpha` differently for each pixel, according to the value in image `#10`. The fit routine also uses `#9` for a baseline.

User variables are defined in the second section of a fitting file as "static" (local to the current file). However, on compilation, all your `xfit.c` files are combined with `fit.c` into one file, so names should be unique among all fitting functions.

Adding New Functional Forms

Additional functional forms can be handled by supplying a C language file that defines the function and how to fit it. Take the following steps to add new fitting functions:

1. Create a file of C source code containing your fitting function. The format of this file is described in detail in "Function Definition Files," page 122.
2. Edit the file `userfit.c` to include your new file.
3. Enter **`make depend`** to update `makefile` to recognize your new file.

   The command `make depend` changes the `makemathfunc` file (a warning `fit.c includes userfit.c more than once!` appears, which is normal). Enter **`make depend`** whenever you change `#include` directives in a file or change the `makefile` itself.
4. Enter **`make fit`** to create the new version of the fit program.

You do not need to exit Image Browser to define new functions. Whenever you click on the Execute button in the Image Browser Math Panel, the current version of `fit` is loaded and executed.

Function Definition Files

By convention, your fitting files should be named `xxxfit.c`, where `xxx` is the type of fit. For example, the file `t1fit.c` is divided into two sections with preprocessor directives:

```
ifdef FUNCSELECTION
first section
#else
second section
#endif
```

The first section contains a fragment of C code that selects the type of fit; several macros are defined to make the job easier. (Macros are indicated by ALL CAPITAL letters.) The following example is taken from `t1fit.c`:

```
IF_FITCODE("t1"){
   N_PARAMETERS = 3;
   FIT_TYPE = NONLINEAR;
   FUNCTION = exp_function;
   JACOBIAN = exp_jacobian;
   GUESS = exp_guess;
```

```
   PARFIX = t1_parfix;
   return TRUE;
}
```

These macros are defined in the following table:

`IF_FITCODE`	Compares your “fit type” string to a given string, and executes the following lines, enclosed by braces, { }, if the strings match. (Case differences are ignored in the comparison.) The bracketed lines show what needs to be done in case of a match.
`N_PARAMETERS`	Set to the number of parameters in the fit. In this case, the number of parameters is fixed, but it could depend on arguments on the Image Browser Math line.
`FIT_TYPE`	Set to one of the following values:
	LINEAR is a function in the following form: `y = C(x) + P0*f0(x) + P1*f1(x) + ...` where `P0` and `P1` are the parameters to be estimated, and the constant `C`, (which might depend on `x`) and the functions `f0` and `f1` of the independent variable `x` are the same for every pixel. LINEAR problems are solved by calculating your “design matrix” (containing the `fn(x)` at each `x`) and inverting it to get a matrix that transforms a vector of observed (`y-C`) values into a vector of parameter values. Thus, matrix inversion needs to be done only once, and the calculation for each pixel simply involves subtracting the constant `C` from the observed `y` values and doing a matrix multiply.
	LINEAR_RECALC_OFFSET is the same as LINEAR, except that `C` can be a function of pixel number. In `y = C(x) + P0*f0(x) + P1*f1(x) + ...` your FUNCTION is called with a zero parameter vector for each pixel in order to reevaluate `C(x)`.
	LINEAR_RECALC is also the same as LINEAR, but now both `C` and the `fn` functions can be a function of pixel number. This means that you must construct a new design matrix and invert it for each pixel.
	NONLINEAR (the default) is used for functions that do not have any of the previous forms. The most desirable functions might be in this category.
`FUNCTION`	Set to the name of the subroutine that calculates the function values. The specifications for this function are on page 124.
`JACOBIAN`	Always optional and is useful only for NONLINEAR functions. It is set to the name of the subroutine (supplied by you) that calculates derivatives of the function with respect to each parameter. If a you do not provide a routine, derivatives are estimated by the nonlinear fit routines. Providing derivatives normally only slightly speeds up fit routines.

`GUESS`	Used only for NONLINEAR functions. It is set to the name of a routine (supplied by you) that calculates an initial guess for the parameter values. Sometimes, fixed initial guesses might work for all sets of data. In such cases, you can omit setting `GUESS` and instead specify default values with the following command `set_default_parameters(3, 0.0, 1.0, 0.0);` where the first argument, `3`, is the number of following arguments; the remaining arguments are the default values. You must provide at least as many values as there are parameters in the fit. If completely fixed guesses do not work, but the same guess can be used for every pixel in the image, you can specify the command `GUESS = fixed_guess;` which allows the initial guesses to be passed on the command line. These guesses would be `n_parameters` constants after the constant for the threshold value.
`USE_PREVIOUS_PARAMETERS`	Used only for NONLINEAR functions. Setting to TRUE should speed up the fit if the routine uses a fixed guess or if the `GUESS` function is likely to be very far off; for example: `USE_PREVIOUS_PARAMETERS = TRUE;` This command means that the first pixel is fit with the values from the GUESS function or fixed guess values, but that subsequent pixels use the parameters from the last successful fit for the guess. If the fitting routine fails with these previous parameters, the GUESS function or fixed guess values are used to try the fitting routine again. This option can speed up the overall fit time by an order of magnitude if the initial guess is not very accurate. For most data, if it is possible to find an initial guess that will make the fit converge (even if it takes many iterations), an initial guess is almost as good as using an accurate guessing function.
`PARFIX`	Set only if the parameters in the functional form specified in the FUNCTION are different from what you want to be reported. This method is used in `t1fit.c`, where the functional form of the fit is `y = P0 + P1 * exp(x * P2)` but the parameters reported are for the fit of `y = P2 + (P1' - P2') * exp(-x/P0')`. Therefore, `t1_parfix` calculates the estimated `Pn'` from the estimated `Pn`, and also calculates new covariances. Writing a `parfix` routine involves extra work, but the routine might be an advantage over having to specify different functions for fits that are equivalent but use different parameters.
`return TRUE;`	Must be entered before the closing brace, `}`.

Additional information can be included before the `return TRUE`; statement, as shown in a fragment of the `shamesfit.c` file in Figure 48. In this fragment, `FIT_TYPE` is made to depend on the number of image vectors passed, and additional numerical parameters on the command line (after the threshold value) are used to set values of variables used in calculating the function. Note that the `nbr_params` variable is set to the number of numerical values on the command line after the threshold value. User variables are defined in the second section as “static” (local to the current file). However, on compilation, all your `xfit.c` files are combined with `fit.c` into one file, so names should be unique among all fitting functions.

The second section in an `xxxfit.c` file contains the user-supplied functions that are mentioned in the first section. First, there is `FUNCTION`, which calculates the values of your fitting function. `FUNCTION` is the only routine needed for any of the varieties of linear fits. It calculates a vector of *y* values given a vector of *x* values and a vector of parameter values. Figure 49 is an example. Note that the `nparams` variable is not used in this routine because `exp_function` is only used for three-parameter fits. If you were fitting an `n`th

```
#ifdef FUNCSELECTION
  IF_FITCODE("shames2"){
    N_PARAMETERS = 2;
    FUNCTION = shames_function;
    switch (nbr_image_vecs){
      case 1:
        FIT_TYPE = LINEAR_FIXED;
        break;
      case 2:
        FIT_TYPE = LINEAR_RECALC_OFFSET;
        break;
      default:
        FIT_TYPE = LINEAR_RECALC;
        break;
  }
  if (nbr_params > 0) alpha = in_params[0];
  if (nbr_params > 1) sbv0 = in_params[1];
  if (nbr_params > 2) hct = in_params[2];
  return TRUE;
}
#else   /* not FUNCSELECTION */

/* Constants for Shames model */
static float alpha=0.136; /* Time Const for [CA-plasma] signal decay */
static float sbv0=0.13;   /* Initial value of [CA-plasma] signal */
static float hct=0.37;    /* Hematocrit */
...
```

Figure 48. Fragment of `shamesfit.c` File

```
static void
exp_function(int npoints,   /* Nbr of data points */
             int nparams,   /* Nbr of parameters-NOT USED */
             float *params, /* nparams parameter values */
             int nvars,     /* Number of indep variables-NOT USED */
             float *x,      /* npoints*nvars values of indep vars */
             float *y)      /* Function values OUT */
{
  int i;
  for (i=0; i<npoints; i++){
      y[i] = params[0] + params[1] * exp(x[i] * params[2]);
  }
}
```

Figure 49. FUNCTION Specifications

order polynomial, for example, `nparams` would specify the order. Similarly, `nvars` is not used because `exp_function` only deals with one independent variable.

`JACOBIAN` is the second routine. Given vectors of parameter values and *x* values, `JACOBIAN` calculates the partial derivative `dy/dp` at each *x* value for each parameter. Note that it returns what looks like the transpose of the Jacobian as it is usually defined.

This transposition is the result of the underlying fitting routines, which are derived from Fortran routines. Compared to C, Fortran stores arrays in transposed order. Figure 50 shows the definition of a JACOBIAN routine.

```
static void
exp_jacobian(int npoints,   /* Nbr of data points */
             int nparams,   /* Nbr of parameters */
             float *params, /* nparams parameter values */
             int nvars,     /* Number of indep variables */
             float *x,      /* npoints*nvars values of indep vars */
             float **dydp)  /* Derivative values OUT*/
{
  int i;
  for (i=0; i<npoints; i++){
    dydp[0][i] = 1;
    dydp[1][i] = exp(x[i] * params[2]);
    dydp[2][i] = dydp[1][i] * x[i] * params[1];
  }
}
```

Figure 50. JACOBIAN Definition

The third routine is the GUESS function, which is required for nonlinear fits and is usually the most difficult routine to define. Accurate first guesses will usually speed up the fit considerably, as well as ensure that it does not converge to a spurious local minimum. Since the guess algorithm is idiosyncratic for each function, you determine how the function is defined. The signature of the function is shown in Figure 51.

```
static int
exp_guess(int npoints,   /* Nbr of data points */
          int nparams,   /* Nbr of parameters-NOT USED */
          float *params, /* Parameter values OUT */
          int nvars,     /* Number of independent vars-NOT USED */
          float *x,      /* npoints*nvars values of indep var */
          float *y,      /* npoints values of dependent variable */
          float *resid,  /* Quality of fit OUT--OPTIONAL */
          float *covar)    /* Covariance matrix OUT--OPTIONAL */
```

Figure 51. GUESS Signature

For an example of a trivial guess function, see `fixed_guess` in the file `fit.c`. Note that the returned values `resid` and `covar` are optional, which means that you must test these pointers to verify that they are nonzero before trying to store values.

TRI_ELEM Macro

The TRI_ELEM macro is provided to easily reference any element of a matrix stored in this format. The syntax `TRI_ELEM(mat,row,col)` references the element of the matrix at the row and column. This macro requires that `row` be greater than or equal to `col`.

The covariance matrix contains only `(nparams * (nparams+1))/2` values, rather than `nparams*nparams`. Only the lower triangle of this symmetric matrix is stored. The storage order is:

```
C(0,0), C(1,0), C(1,1), C(2,0), C(2,1), C(2,2), C(3,0), ...
```

PARFIX Routine

With PARFIX, estimated parameters can be combined to form estimates for other parameters that were not explicitly fit. There are some potential pitfalls involving the covariances between parameters. For example, the estimate of the sum of two parameters is

```
E[p0 + p1] = E[p0] + E[p1]
```

but, the estimated value of their product is

```
E[p0 * p1] = E[p0] * E[p1] + Covar[p0, p1]
```

This value is the direct result of the covariance definition. Because calculating the variance of the newly synthesized parameters can be fairly complex, avoid using PARFIX routines. Instead, directly write functions in terms of the parameters you actually want to know.

5.5 Problems with Image Browser Math

You should be aware of the following Image Browser Math problems.

Run-time Errors

Image Browser has no automatic run-time validation of math operations, so you must check data values, as shown in these examples:

```
#1=(#2==0)?0:#1/#2
#2=sqrt(fabs(#1))
#5=(#1<=1.0e-6)?log(1.0e-6):log(#1)
#5=log(#1<1.0e-6?1.0e-6:#1)
```

If a function that you create has bugs (such as using uninitialized pointers) that result in memory violations, the entire Image Browser program is core dumped. Core dump files result because, while your function is running, it is actually part of Image Browser.

CAUTION: **Before performing possibly illegal operations, check data values.**

It is also possible to write Image Browser Math Expressions, like the following, that will kill Image Browser:

```
#2 = #1 + *(float *)0
```

CAUTION: **Be careful when programming and testing new user functions.**

Run-time error messages can be found in the window from which Image Browser was started and a core dump file can be in the directory from which it was started.

Compilation Errors

If an illegal expression is entered, Image Browser does not generate a legal C program and the Error Messages window displays:

```
Math: Program did not compile
```

Compiler errors are also written into the window from which Image Browser was started. Unfortunately, these messages might be of limited use because the C program source is not available for inspection.

Chapter 6. CSI Data Processing

Sections in this chapter:

CSI Data Processing is a tool, based on the X Window System, designed for the easy processing of chemical shift image (CSI) data. It uses mouse-oriented, point-and-click methods to execute selection and processing requests.

The CSI tool was designed to process CSI data to obtain metabolic maps, but other outputs can be obtained: localized FID data, multivoxel spectra, individual spectrum, and pH maps. Input to the CSI tool is expected to be 2D CSI or image (for reference images) data in the Varian VNMR raw data (FID) format. CSI or image data can be imported and processed as long as the data is formatted to the specifications of the Flexible Data Format (FDF).

6.1 Overview of CSI

This section describes the system requirements for operating the CSI tool, the CSI screen layout, processing and graphics functions used by CSI, display controls, and data formats.

System Requirements

CSI operates on platforms with the following configuration:

- Sun SPARC computer
- 8-bit, 24-bit frame-buffer
- OpenWindows and higher
- Solaris 2.3 or higher

The minimum memory requirement is 12 MB; however, more that 16 MB is recommended to enhance performance. CSI does not take advantage of 24-bit color.

Swap space is also a factor because CSI data sets can be very large. Three times the memory size in swap space is recommended.

Screen Layout

The overall layout of the CSI screen is shown in Figure 52.

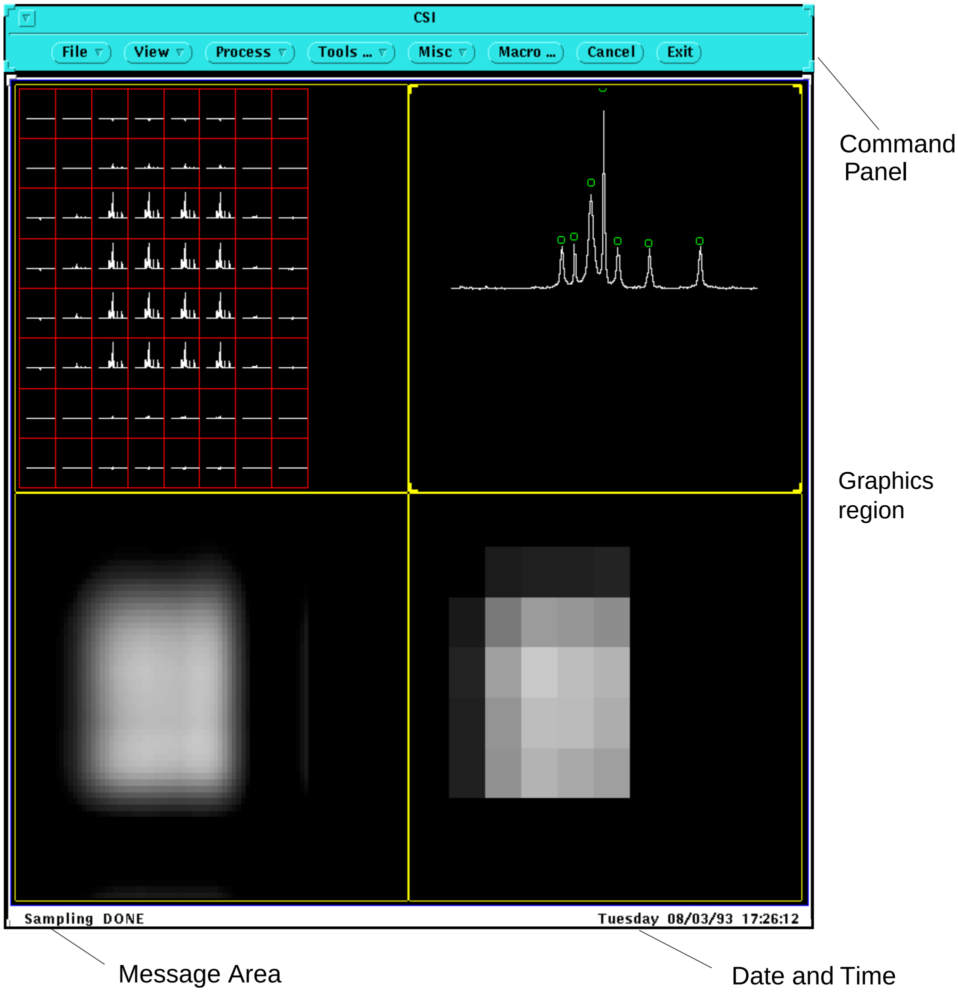


Figure 52. Default Layout of Main CSI Windows

Command Panel

The command panel contains command menus where specific operations can be invoked, such as process data or display an image or another window.

Graphics Region

The graphics region occupies the largest portion of the screen, and can be directly interacted with the mouse. All graphical drawings and images are shown inside the graphics region. The region can have a number of graphics frames where CSI data, spectra, and images are displayed.

Before data can be displayed, a graphics frame must be created somewhere in the graphic region. Data is automatically resized to fill the graphics frame. CSI and image data keep their aspect ratio. Besides displaying data, region of interest (ROI) tools and markers can be created, lines can be drawn, and text written in the graphics frame.

Message Area, Date and Time

Below the graphics region, informative messages are displayed on the bottom bar of the window frame. This is the standard way of displaying messages in the OPENLOOK user interface. Error messages are displayed in a separate window. The date and time are displayed in the lower-right corner.

Processing Functions

When using the CSI tool, it is best to think of it as a series of processing steps used to process and manipulate CSI data to obtain multivoxel spectra (MVS) data, metabolic maps, and pH maps (or frequency difference maps). Supporting these processing steps are interactive tools, input/output tools, and viewing tools that make these steps easier.

Figure 53 shows the data flow through the main processing functions. The circles represent processing operations and the squares represent data. Note that the data can be saved after each operation and retrieved for the next operation. Also, note that phase and baseline correction processing can be iterated.

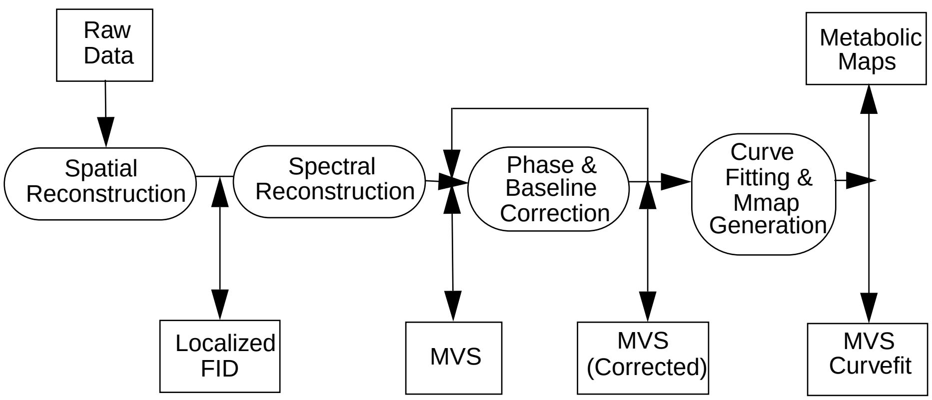


Figure 53. Processing Functions Data Flow

The data is saved in global buffers after each processing step. Data can always be redisplayed or reprocessed with an earlier step.At any time during these operations, a reference image can be processed and displayed with the current localized FID, MVS, or MVS curve fit data overlaid.

Other processes not shown in the diagram can be performed. These processes include peak arithmetic, pH maps, and frequency difference maps.

Spatial Reconstruction	Performs a Fast Fourier Transform (FFT) on the input raw data to obtain a set of localized FID voxels. This set can be in one or two dimensions. Weighting functions and zero-filling can be applied to the data. Voxel shifting can also be performed on the data.
Spectral Reconstruction	Performs an FFT on the localized FIDs generated by spatial reconstruction to obtain the multivoxel spectra (MVS) data. Weighting functions can be applied to the data. zero-filling can be applied before and after the data.
Phase and Baseline Correction	Perform phase and baseline correction on the spectra. Correction can be done manually or automatically on a spectrum-by-spectrum basis or automatically on all the spectra in the MVS data.

Metabolic Map	Generates a metabolic map from the MVS data. The data must be curve-fitted before metabolic maps can be generated. curve-fitting can be done on a local or global basis.
Image Reconstruction	Allows reference images to be reconstructed from raw data.
Image Calctool	Does calculations using spectral peaks for generating metabolic maps by using combinations of peaks and scalar values.
pH Map	Calculates pH maps and frequency difference maps between selected peaks in the spectra.
ROI Spectrum	Extracts a series of spectra along a defined line or extracts an averaged spectrum from inside a rectangular ROI.

Graphics Functions

Tools are provided to allow the creation and modification of various types of objects in the graphics region. CSI uses the same tools as ImageBrowser: Frame, Zooming, Vertical Scaling and Contrast, ROI, and Text Annotation. However, CSI has some differences from ImageBrowser: CSI only implements box and line ROIs, and has added graphics functions to perform voxel selection of spectra, peak picking, curve fitting, and interactive filtering.

The ImageBrowser standard colormap uses an 8-bit frame buffer, which can show only 256 colors or gray levels at a time on the screen. The default structure is as follows:

grayscale	64 levels	miscellaneous	12 levels

CSI uses a colormap different from the standard colormap for overlaying metabolic maps over a reference image. Its structure is as follows:

Display Control

Use the Tools and the View command panel options to control the CSI display, including images and spectra.

grayscale	64 levels	bluescale	27 levels
redscale	27 levels	miscellaneous	12 levels
greenscale	27 levels		

Various image display parameters can be manipulated with some of the graphics tools. For example, Vertical Scaling controls the intensity and contrast of the display, and the Zooming tool allows magnification on individual spectra.

The View submenus in CSI provide viewing of localized FID, MVS, curve fit data sets, and generated maps overlaid on reference images. These viewing requests are useful because all the data is kept in global buffers, but many times the display of the data has been overwritten. These viewing requests allow the stored data to be reviewed.

Displaying and redisplaying overlaid images on CSI data sets is useful for drawing and getting ROI information by using the reference image.

The Colormap option in the View menu allows up to three different metabolic maps (using red, green, blue intensity scales overlaid on a grayscale reference image) to be displayed.

One of the options in the View menu is Properties, which allows some of the display functions, including fixed or automatic scaling of spectra, to be customized.

Data Formats

CSI supports two data formats:

- *VNMR raw data (FID)* **–** Format that enables reading raw CSI data for processing or raw image data for image reconstruction.
- *Flexible Data Format (FDF)* – Format that CSI uses to output all data. CSI adds fields to the original FDF specification. Localized FID, MVS, reference images, and metabolic map data can also be read in this format.

The CSI product has utilities that allow FDF files to be created from other data files.

6.2 Getting Started

This section describes the process of verifying the correct user environment, starting CSI, and performing some of the basic functions.

Setting the User Environment

CSI has been designed to run in an X Window System environment. This means that any X terminal can be used as the user interface as long as it supports the 8-bit graphics. The host system that actually runs CSI must be a Sun workstation with Solaris 2.3 or higher.

Host systems should have as much memory and swap space as possible. CSI data sets tend to be very large and, after each processing step, the data set is saved in memory.

Environment Variable

The `CSIDIR` variable contains the directory path to the user's initialization directory. The following command should be in your `.login` file:

```
setenv CSIDIR $HOME/csi_initdir
```

If a new user is created with the `makeuser` script, this variable is automatically set. `CSIDIR` points at a user initialization directory.

Initialization Directory

The initialization directory in `/vnmr/user_templates` contains files, bitmaps, frame directory, ROI directory, and PEAK directory used for starting up, tuning, and running CSI. This directory is copied into the user's home directory when `makeuser` is run. It can be copied into any location within the user's area as long as the environment variable `CSIDIR` is set to point to the new location. Within the initialization directory, all files ending with the suffix `.bm` are bitmap files and must not be changed.

The initialization directory contains the following relevant files and directories:

`colormap.init`	Contains the colormap definition. Colors for graphics frames (Gframes) can be defined, as can ROIs and text annotation fonts.
`window.init`	Contains the default positions for the main CSI window and various subwindows.
`csiparam.init`	Contains processing factors and parameters for tuning certain CSI processing functions.

`gframe`	Directory containing graphics frames layouts. The file with the name `default` is the set of Gframes that are loaded at bootup. This is the directory where sets of Gframes can be saved. A personal default set of Gframes can be created by overwriting the current `default` file.
`roi`	Directory where any created ROIs for loading onto a set of images can be saved.
`PEAK`	Directory containing peak information files for peak picking and curve-fitting using prior knowledge. Personal prior knowledge files can be inserted here.
`macro`	Directory containing user macros and, in particular, the macro `startup`, which is executed when ImageBrowser starts. `startup` might load a set of Gframes and set various options, such as the gamma correction settings.

Starting CSI

CSI is started with the command `csi`, which actually starts two processes. One process runs the CSI command panel and is named `csi`. The other process controls everything else, including the processing and graphics, and is named `P_csi`.

When CSI starts, it reads the `colormap.init` and `window.init` files to initialize the colormap and the window locations and sizes on the screen. It also executes `startup` in the file `$CSIDIR/macro/startup`.

Before manipulating frames and loading images, you need to know how the mouse buttons and the command panel menus function, because CSI is a point-and-click based tool.

Using Mouse Buttons

Details about mouse buttons use can be found in the *OpenWindows Version 2 User's Guide*. In general, mouse button use can be summarized as follows:

Left button: SELECT

Inside the command panel, the left mouse button is used to invoke commands.

Inside the graphics region, the left button is used to select an object or to draw an ROI or to annotate text. Selecting an object deselects any previously selected objects. Objects that can be selected include graphics frames, voxels, ROIs and markers, and text. The object selected is chosen according to a priority hierarchy:

1. If the cursor is inside an ROI, near a line or point ROI, or near text, the corresponding object is selected. If there is more than one qualifying object, only the most recently created object is selected.
2. If the cursor is inside a frame boundary, the frame is selected.

The shape of the cursor changes when different graphics tools are selected, to identify which operations the mouse is ready to perform.

MIDDLE button: ADJUST

The middle button of the mouse is not used inside the command panel.

Inside the graphics regions, the middle mouse button toggles the state of an object, selecting it if it is not selected and deselecting it if it is.

RIGHT button: MENU

The right mouse button is used to open menus in the command panel.

Using FileBrowser

The FileBrowser tool for loading files is the default choice when the command panel File option is selected. The initial FileBrowser directory is the directory where CSI was started. A file or directory is selected when the name is highlighted in the scrolling list or when the name appears on the top line of the FileBrowser.

To change directories, either double click on a directory selection or click on a selection to put the directory name onto the top line and then press the Return key. The full directory name also can be typed, followed by pressing Return. The ~ identifier operates the same as the in the C Shell.

CSI loads VNMR data files differently than ImageBrowser:

- To load a phasefile in ImageBrowser, select the directory containing the phasefile, then select LOAD.
- To load raw data In CSI, move to the directory where the `fid` file is located, select the file named `fid`, then select LOAD.
- To load FDF files, select the file with the data, then select LOAD.

See "Files and Other Items," page 104 for a more complete description of the FileBrowser.

Using Command Panel Menus

Figure 54 shows the command panel with its set of basic command options.

Figure 54. CSI Command Panel

Options with an arrow (▽) have menus that are activated by the right mouse button, or the left mouse button can be used to select the default choice. The action of these submenus can process data, open a window, etc., depending on the functional operation.

Most functions are self-explanatory and are explained in this section or later in other sections of this manual.

Creating and Manipulating Graphics Frames

Graphics frames are a variety of graphics objects. Perform the following steps to create and manipulate frames.

Opening the Graphics Tools Window

- Open the Graphics Tools window, shown in Figure 55, by clicking on the Tools option with the left mouse button.

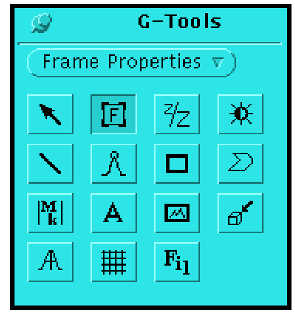


Figure 55. Graphics Tools Window

Selecting Frame Functions

Select the Frame option  when performing any of the frame functions other than simply selecting a frame.

1. To see the Frame Properties menu, position the cursor over the Frame Properties button and hold down the right mouse button. Frame-related commands and options are displayed.
2. Hold down the right mouse button and move the cursor down the list of options shown in Figure 56 to select a command. When the desired option is highlighted, release the button to select it.

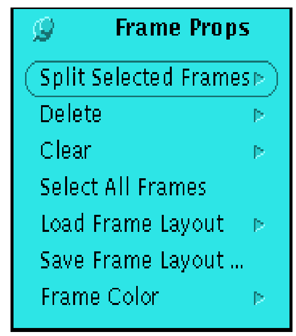


Figure 56. Frame Props Window

Deleting Gframes

If the setup of the Gframes on the screen is unsatisfactory, select the Delete option in the Frame Props menu to remove all frames on the screen.

Creating Gframes

1. Position the cursor in the graphics window and hold down the left mouse button.
2. Drag the cursor across the screen. A box is created.
3. When the left mouse button is released, the box is completed and selected. Frames cannot overlap any part of another frame.

Selecting Gframes

1. Position the cursor within the frame and click the left mouse button. The frame's corners become highlighted to show that it is selected; any other selected frames are deselected.
2. Use the middle mouse button to select additional frames.

   Clicking on a frame captures it if it was not already selected or releases the frame if it was already selected. There is also a menu selection in the Frame Properties menu that selects all Gframes.

   You do not need to click on the Frame option  to select and deselect Gframes. Use the Zooming G-tool to choose a frame with the left mouse button. You can use the ROI G-tool to select frames with the left mouse button and toggle between selections with the middle mouse button; make sure the cursor is not in an ROI. You can also use Voxel Select, Peak Select, and Annotation to select frames.
3. To select a number of Gframes, click on the Frame option in the graphics tools menu shown in Figure 55. Select each frame with the middle mouse button to append each frame to a selection list.

Moving Gframes

1. Select a frame, then position the cursor within the selected Gframe.
2. Hold down the left mouse button and drag the frame to a new location.

Resizing Gframes

1. Select a frame, then position the cursor on the desired highlighted corner.
2. Hold down the left mouse button and drag the corner to the desired position.

Splitting Gframes

Graphics frames can be split into a number of smaller frames, which allow viewing formats to be easily and quickly set up. To split a Gframe, do the following steps:

1. Activate the Frame tool.
2. Select the Gframe or frames to be split.
3. Select the option Frame Properties.
4. Select the option Split Selected Frames.
5. Choose the desired split (1x2, 1x3, 1x4, etc.).

Storing and Retrieving Gframes

You can store and retrieve Gframes by clicking on the Save Frame Layout and Load Frame Layout options in the Frame Props menu, shown in Figure 56. The files are stored into, and retrieved from, the `$CSIDIR/gframe` directory or a subdirectory. Gframes are retrieved with the same size and positions with which they were stored. They are not adjusted to fit the size of the graphics window. Frames that are entirely outside the current graphics region or overlap with existing frames are not loaded.

The Save Frame Layout menu selection saves all currently selected Gframes. It switches the FileBrowser to graphics-frame save mode. Use the FileBrowser to change to the desired directory and save the frames.

Clearing Gframes

Use the Clear command in the Frame Props menu, shown in Figure 56, to erase the contents of all frames, selected frames, or unselected frames.

Loading Data

To load data, select the File option. The window CSI File Handling Tool opens in data load mode. Directories and data files can be browsed, and the desired data set can be loaded. CSI accepts two types of data formats: Flexible Data Format (FDF) and VNMR raw data (FID) format. Simulated data can also be generated. Data simulation allows processing and graphics functions to be tried without having to acquire data.

Generating Simulated Data

The CSI tool can be used without collecting data. CSI can generate simulated data with truncation effects (Gen.Data.Truc) or with basically clean data (Gen.Data.Cont.) These data types can be selected from the command panel File option.

A reference image is generated along with the CSI data. The CSI data that is simulated is P31 data.

VNMR Raw Data Files

CSI is made to process raw CSI data, which is generally assumed to be in the VNMR raw data file format. This data can be retrieved by descending into the directory that contains the FID file, selecting `fid`, and then selecting Load.

Double clicking on the directory, or pressing Return after its name, does not load the data; it opens that directory.

For example, to analyze VNMR CSI data in `exp3`, start CSI, open the FileBrowser, double click on directory names until the `../vnmrsystem/exp3/acqfil` file appears, select `fid`, then select Load.

Remember that file loading in CSI is different from file loading in ImageBrowser. To load files in ImageBrowser, specify the directory in which VNMR phasefiles are to be stored, and then select Load.

FDF Files

CSI can store data as FDF files at intermediate steps for later processing. This data, along with other data that can be more easily imported by using the FDF format, can be loaded with the FileBrowser. An FDF file can be loaded by double-clicking, by selecting the file and pressing the Return key, or by selecting the file and selecting Load.

Storing Data

Data can be stored at intermediate steps while it is being processed. Figure 53 on page 131 contains a data flow diagram that shows at what points during processing that data can be saved.

CSI data is easily stored by clicking the right mouse button on the File option in the command panel, and then selecting Save. The FileBrowser window opens in the data save mode, or else the current FileBrowser window is changed to that mode. As with Load, FileBrowser opens with the directory in which CSI was started. Choose a directory, a file name, and select Save. CSI opens a menu prompting for the type of data to be saved.

This process is different from ImageBrowser, which saves the data in the currently selected Gframe. CSI keeps global data buffers that might not be currently displayed, but the data is processed and saved. All data is saved as FDF files. See “Processing Functions,” page 156 for more information about data processing.

Using Graphics Tools

The graphics tools or G-Tools window is opened by selecting the Tools option in the command panel. The graphics tools window opens with the Frame tool as the default tool.

Graphics tools are mostly used to support the following processing functions:

- ROI manipulation
- Gframe manipulation
- Zooming
- Vertical scaling (scales the data to the pixel display values)
- Line ROI drawing

- Peak or baseline markers
- Box ROI drawing
- Vertical line markers
- Text annotation
- Interactive phasing and spectrum scaling
- Voxel selection
- Curve fittings
- Interactive weighting/filtering

A tool is activated by pointing to it with the cursor and clicking the left mouse button. After a graphics tool is activated, items can be selected or dragged by using the left mouse button. Commands can be performed by clicking on the properties option above the graphics buttons with the right mouse button. Typical commands are Load, Save, or Delete in the case of Gframes or ROIs; and Zoom or Unzoom in the case of zooming.

See “Tools,” page 147 for a description of graphics tools that support CSI data set processing.

Processing a CSI Data Set

To acquaint you with processing CSI data, this section describes the CSI data set processing. In the example used in this section, the data is simulated data.

To view the processing steps that need to be performed, compare Figure 57 with the data flow diagram in Figure 53. Both figures show the processing steps that must be taken after the data has been read in.

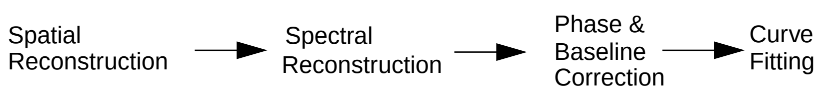


Figure 57. CSI Data Basic Processing Steps

Generating Simulated Data

The first step is to generate data, which can be read in by using the FileBrowser. However, in this case, simulated data is used. Select the Gen.Data.Cont entry in the File menu with the right mouse button. An 8-voxel-by-8-voxel phosphorus data set is generated.

Note that nothing is displayed. Only a message in the bottom left corner indicates the data has been generated.

Spatial Reconstruction

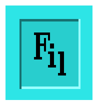
Select the Process option in the command panel to open the Spatial Reconstruction window. It can also always be opened from the submenus with the right mouse button. The menu appears with default values specified in all the fields.

Select the Apply option in the Spatial Reconstruction window to process the raw data and display the localized FID data in the currently selected Gframe.

The processing parameters associated with spatial reconstruction are zero-filling, filtering, voxel shifting, and rotation. To use a parameter, change the desired field or fields and select

the Apply option. The data set is reprocessed and the localized FID is redisplayed in the currently selected frame. The default graphics tool is the frame tool. To select another Gframe for displaying, position the cursor in another frame and click the left mouse button.

Filtering or Weighting



The Filtering (or Weighting) tool, described on page 156, is available, but its use is limited with spatial reconstruction. The reconstruction of one line of data in the spatial dimension can only be looked at. However, a filtering function can be looked at and constructed.

To use the tool, select an empty Gframe. Select Tools, Graphics, and then the Filtering tool. The selected Gframe splits into three sections, as shown in Figure 58.

To manipulate the filtering function (middle window), press the left and middle mouse buttons. All parameter changes appear in the Spatial Reconstruction window. Parameters can also be changed in the window; changes appear in the filter Gframe.

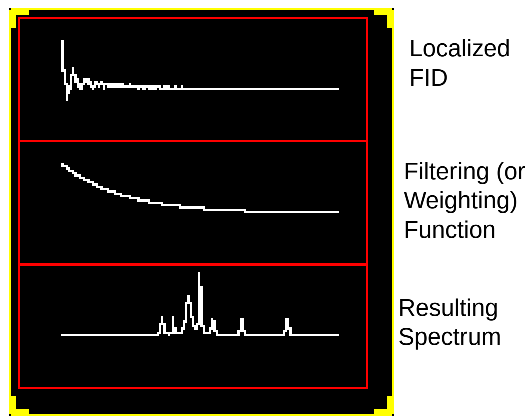


Figure 58. Filtering Display

Spectral Reconstruction

After spatial reconstruction has been completed, select the Process option in the command panel to open the Spectral Reconstruction window. The window can also always be opened from the submenus with the right mouse button. The window appears with default values specified in all the fields.

Select the Apply To All option to process the localized FID data and display the MVS data in the currently selected Gframe.

Processing parameters associated with spectral reconstruction are zero-filling, filtering, and left- or right-shifting of the FID. To reprocess the data set and redisplay the MVS data in the currently selected frame, change the desired field or fields and select the Apply To All option.

Filtering or Weighting

The Filtering (or Weighting) tool is fully available for use with spectral reconstruction. The effects on a selected spectrum can be seen by using different weighting functions (pre-zero-filling and post-zero-filling) before applying the processing parameters to the entire data set. To use the tool, select a Gframe, load a spectrum into the Gframe, and select the Filtering tool. The filtering display in Figure 58 appears.

A localized FID can be loaded either by using the Voxel Pos. field and Load option in the Spectral Reconstruction window or by using the Voxel Select tool , described on page 154, in the G-Tools window. The following example describes how to use the Voxel Select tool.

1. Select the Voxel Select tool in the G-Tools window.
2. Move the cursor to an empty Gframe and capture it with the left mouse button.

3. Move the cursor over a voxel in the previously processed Localized FID grid, and click the left mouse button. The FID from that grid appears in the selected Gframe.
4. If the Localized FID display has already been overwritten by the MVS display, use the walking menus of the View option in the main command panel to redisplay the Localized FID display.
5. After the FID is in the selected Gframe, select the Filtering tool in the G-Tools window.
6. Use the left mouse button, then the middle mouse button within the filtering window to select filtering (weighting) functions in the Spectral Reconstruction window and interactively manipulate the shape of the filtering function (middle window).

Zero-filling can be accomplished by increasing the Point f1 field. Left-shifting or right-shifting of the FID can be accomplished by using the Delay field. All parameter changes appear in the Spectral Reconstruction window. Parameters in the window can also be manipulated; the changes appear in the filter Gframe.

Phase Correction

After spectral reconstruction, phase correction is the next step in CSI data processing. Most of the time automatic phase correction can be used. A phase can be adjusted globally, on a subset of the voxels, or voxel by voxel.

Automatic

1. Open the Phase Correction window, shown in Figure 59, and select Both in the Phase Order field for Const and Linear phase correction.
2. Select the Automatic mode for Global Phase Correction and click Apply to All.

Write All

If a large linear phase correction is needed or if autophasing is not giving the desired results, the following procedure can be used.

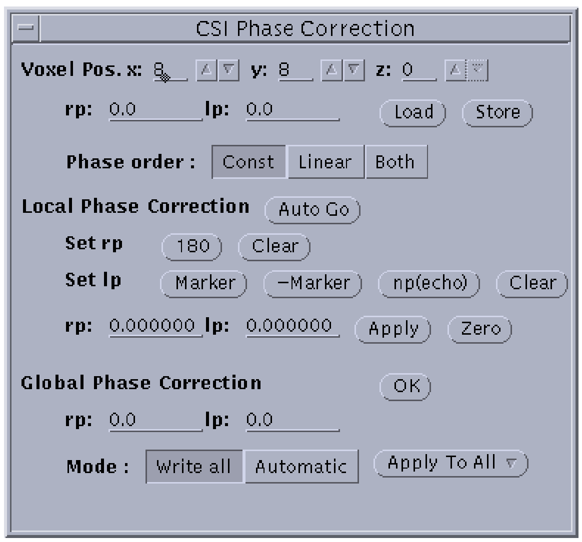


Figure 59. Phase Correction Window

1. Select a spectrum from the just processed MVS data.
2. Select the desired phase order option; then select Auto Go, directly set the phases, or use the spectrum tool.

To apply the phase values to the entire data set, perform the following procedure:

1. Select the OK option in the Global Phase Correction field.
2. Select Write All.
3. Select Apply To All.

After registering the values, you can wait to update the data set and apply the phase and baseline corrections at the same time.

To skip the previous procedure, select the Automatic option in the Mode field.

Adjusting the Phase with the Spectrum Tool

If the automatic phase adjustment is not making the desired phase adjustments, the Spectrum tool  , described on page 154, in the G-Tools window can be used. After a spectrum has been selected, select the Spectrum tool. The default type of phasing is constant phasing; however, this method can be changed by clicking on the Filter Properties option in the G-Tools window. After the type of phasing has been selected, the phase can be manipulated by positioning the cursor over the spectrum, holding down the left mouse button, and moving the cursor up and down within the Gframe.

After the desired phasing has been reached, select the Auto Go option in the Local Phase Correction field to register those phase values, then select Write All.

Baseline Correction

The same as with phasing, the procedure to apply a baseline correction to the data can be skipped if desired.

Baseline correction is performed in a similar manner to phasing, but different functions and tools are used. Click on Baseline Correction in the Process menu (see Figure 60). Select a spectrum and perform the correction on it before operating on the entire data set. There are three methods for baseline correction:

- Spline
- Polynomial
- SINC

For faster performance in baseline correction, select Write all mode in the Global Baseline Correction field. The Automatic mode can take tens of minutes. To register the correction values for the Write all mode, select Correction OK after the sampled points and the correction method are satisfactory, then select Apply To All.

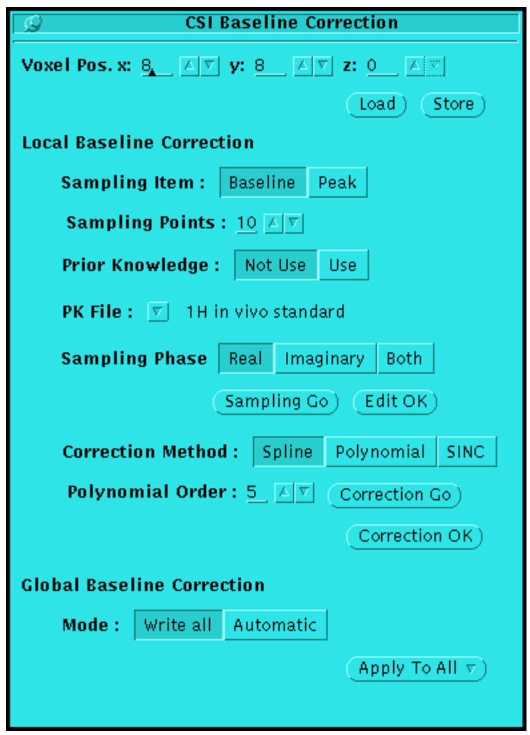


Figure 60. Baseline Correction Window

Baseline Sampling

With Baseline sampling as a default, select the Sampling Go option. A baseline sampling on the spectrum in the selected Gframe is performed and a number of sampling points are displayed. If these sampled points are satisfactory, choose either the Spline or Polynomial correction method, then select Correction Go. The corrected spectrum is displayed in the current Gframe with the baseline curve used for correction overlaid on it.

If the sampled points are not satisfactory, points can be added by performing the following procedure:

Add Points

1. Select the Picking tool , described on page 155, and insert a point at the desired location on the spectrum by clicking the left mouse button on the mouse.
2. After you add a point, the G-Tools window defaults to the ROI Select tool described on page 153. To add more points, select the Picking tool again.

Move Points

To move points, do the following procedure:

1. Select a point with the ROI Select tool.
2. Hold down the left mouse button, and move the cursor/marker to the desired location on the spectrum.

Delete Points

To delete a point, do the following procedure:

1. Select the point.
2. Select Delete from the Picking tool Marker Properties menu.

Make the Correction

When you are satisfied with the points, do the following procedure to apply the edits:

1. Select Edit OK.
2. Make sure the correction method is either Spline or Polynomial, then select Correction Go.

Peak Sampling

Peak Sampling can be performed by selecting Not Use or Use in the Prior Knowledge field. Prior Knowledge is usually desirable. If it is used, the correct Prior Knowledge (PK File) file must be selected. In this case, it is the 31P in vivo standard. The PK files can be viewed and selected by using the right mouse button. Select Prior Knowledge Use and PK File 31P in vivo standard, and then select Sampling Go. A marker should appear on each peak. If no markers appear, they can be added using the picture tool.

If the markers are properly positioned, make sure the SINC correction method is specified, and then select Correction Go.

Metabolic Map Calculation

To calculate the metabolic map information, the CSI spectral peaks must be defined, and, if desired for more accurate information, curve fit. This is the last standard processing step. Select the Metabolic Map option from the Process menu to open the CSI Metabolic Map Calculation window (see Figure 61).

At this point, the peaks must be specified for curve fitting. This must be done on a local spectrum, so as in the previous processing steps select a spectrum from the CSI display.

Local Peak Picking

The CSI tool works best when Prior Knowledge is used. Select Prior Knowledge Use and PK File 31P in vivo standard and select Sampling Go. A marker should appear on each peak. If they do not, it may be necessary to select the Picking Tool from the G-Tools window to manually specify any missed peaks. If there are markers on each peak, you can move on to the Local Specification.

The peak information is displayed in the Info Messages window.

Local Mmap Specification

To define the Mmap peaks and curve-fitting parameters, select the Specify CurveFit and Mmap button, which opens the Interactive Curve Fitting window.

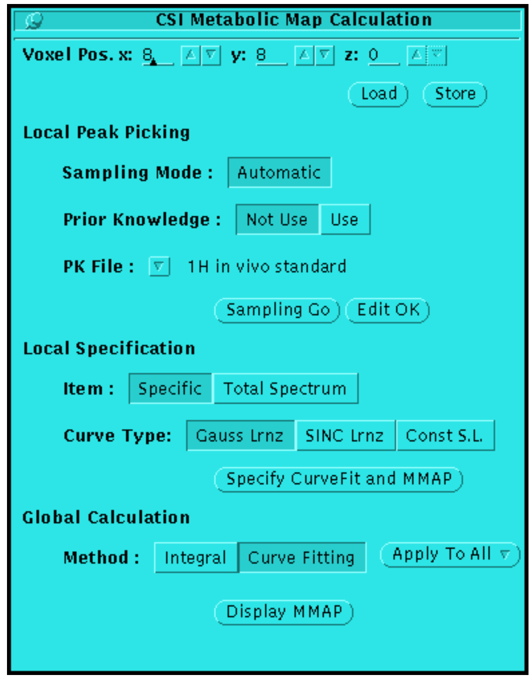


Figure 61. Metabolic Map Calculation

Interactive Curve Fitting

When the interactive Curve Fitting window opens, a curve fit of the first peak is overlaid on the spectrum in the selected Gframe, along with cross-hair markers on each peak. The curve fit parameters for the first peaks are displayed in the window. Step through the peaks on the panel. Each time a new peak is selected, its curve fit is overlaid on the spectrum.

If all the curve fits look okay, register the peaks and the metabolic maps by selecting the Peak Registration and Mmap No. Set options.

Perform a curve fit of the entire spectrum by selecting Auto Curve Fit. If the curve fit is satisfactory, select Fitting OK to close the interactive Curve Fitting window. Remember, the peaks must be registered and the Mmap numbers must be set before closing the Interactive Curve Fit window. Otherwise, the Global Calculation does not work correctly.

To adjust the fitting parameters, place the cursor on one of the peaks. To better adjust the cross-hair cursor, zoom in on the selected peak. After adjusting one or all of the ends of the cursor, select the Edit from Marker option on the panel to update its values. Select the Curve Check option to update the fit.

Global Calculation

After the peak and metabolic map numbers have been registered, select either the Integral or the Curve-fitting method and then the Apply To All button in the Global Calculation field.

Integral Method

The Integral Method is the fastest way to get Mmap information. It finds the peaks in a voxel and calculates the area under the peak. However, if there are two peaks close together,

the integral method does not find all the area under the peak. It only gets the area directly under the peak, and when the second peak starts, this method starts integrating the area under it. When this situation occurs, the Integral Method can give misleading results. However, it can be useful to see which peaks are being picked up over the entire set of voxels.

Curve-Fitting Method

Global curve fitting generally takes a long time. If you are only be interested in a localized region of the CSI data, you can do the following:

1. Select your destination Gframe, which can be the last MVS data Gframe. T
2. Select the Box ROI tool  , described on page 154, in the G-Tools window.
3. Draw a box through the desired voxels. Any voxel lying within or on the ROI boundaries is selected.
4. When you are satisfied with the selected region, select the Apply To All option.

Figure 62 shows the selected voxels with box ROI (left side) and the resulting curve fitted display (right side).

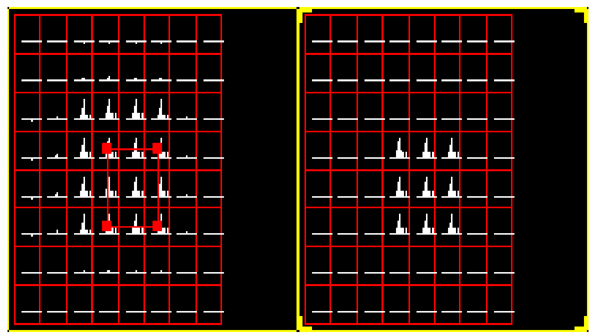


Figure 62. Selected Voxels and Curve-Fitted Data

Metabolic Map Display

Figure 63 shows the data flow for metabolic map processing.

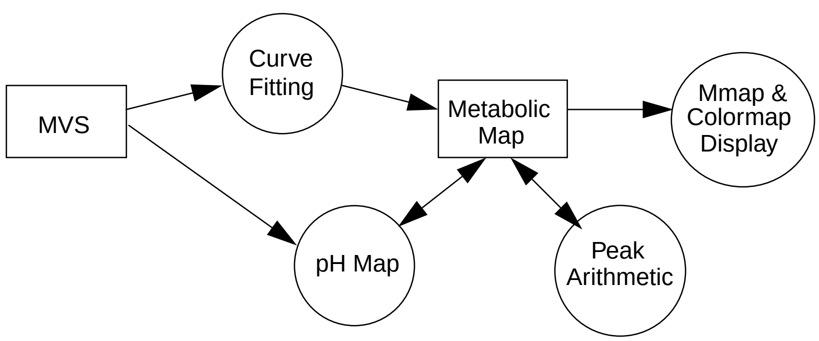


Figure 63. Detailed Data Flow for Metabolic Map Processing

When the data is fitted and the metabolic maps based on the peaks have been registered, the maps can be displayed either by using the Display Mmap option in the CSI Metabolic Map Calculation window or by clicking Colormap in the View option in the command panel.

Both menu panels are straightforward. Select a frame, a peak, and the display option. The images can be interpolated to provide a smoother image. The Display Mmap Info option shows a list of the register maps in the Info Messages window.

The Colormap Display window allows up to three metabolic map images using RGB colors to be simultaneously displayed and overlaid on a reference image, if desired. See “Image Reconstruction,” page 165 for instructions on creating a reference image. For this simulated data, however, a reference image was created along with the CSI data and can be displayed along with the Mmaps by using the Colormap Display window.

Image (Peak) Arithmetic

Peaks can be operated on to form new peaks, which can be saved and displayed as new maps. Perform the following steps to run the Image Arithmetic process:

1. Use the right mouse button to select Process from the command panel, then select Image Calctool.
2. Select a Gframe.
3. Use the cursor and the left mouse button to enter an arithmetic expression such as `1-2=8.` This expression subtracts peak two from peak one and creates a new peak 8. Select the Return option ↵ to run the calculation.

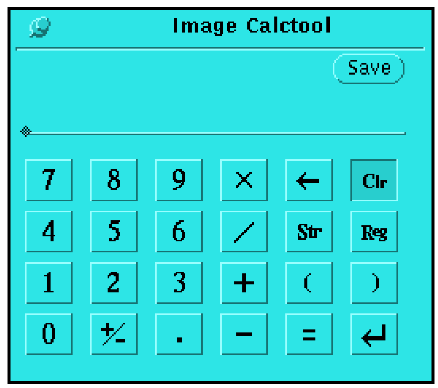


Figure 64. Image Calctool Window

When ↵ is selected, a new map is formed and displayed in the selected frame by using the arithmetic expression. But, the map is not registered or saved as a metabolic map display peak until Save is selected. Figure 64 shows the Image Calctool and Figure 65 shows the Save Check window.

Note that the 8 as a result in the expression was optional, and nothing needed to be placed to the right of the = sign. When Save is selected, a window (allowing the map number and a comment field to be specified) opens. Enter something in the comment field that allows you to later recognize the map.

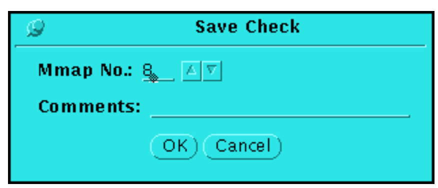


Figure 65. Save Check Window

pH Map

Calculate pH maps and frequency difference maps from the MVS data or the metabolic map data by performing the following steps:

1. Select pH Map from the Process option with the right mouse button.
2. Select a Gframe.
3. As an example, create a default pHmap. Select Mmap in the Peak Define field.
4. Select the Mapping Apply option to display a pH map in the selected Gframe.

Nothing is registered or saved until Save Map is selected, which opens a save window (that again allows the map number and a comment field to be specified).

See "pH Map Control," page 166, for more information on pH and frequency difference maps

Box ROI Tool

The Box ROI tool draws a rectangular ROI. It is used in the statistics processing function.

To draw a rectangular ROI after the tool is selected, position the cursor at one of the desired corner coordinates, press the left mouse button and drag the cursor over the desired region of interest area. As the cursor is being dragged, an XORed rectangle is drawn. When the left mouse button is released, the completed rectangle appears in the selected ROI color.

6.3 Tools

This section describes the graphics tools listed in the Tools menu.

Graphics Tools

Figure 66 shows a Graphics Tools (G-Tools) window. This window contains a set of tools to create and manipulate objects (or an image inside an object), and to annotate text on images.

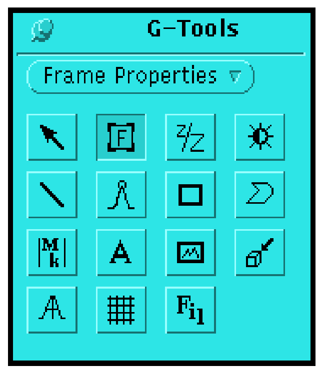


Figure 66. Graphics Tools Window

Choose a tool with the left mouse button. Only one graphics tool can be active at a time.

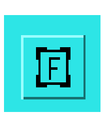
In addition to graphics tools, the Frame Properties option activates a pulldown menu listing several options such as split, save, and load frames. The properties menu changes according to the individual function of the selected graphics tool.

The following sections describe the functions of graphics tools. Mouse use to select, create, move, or resize graphic frames or text is not described here (See the *OpenWindow Version 2 User's Guide* for mouse use related to graphics).

Graphics Frame Tools

This section describes the functions of graphics tools for creating, zooming, and scaling graphics frames.

Frame Tool



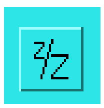
The Frame tool creates a graphics frame. A graphics frame is used to indicate the position and size of an image on the screen.

An image can only be displayed inside graphics frame. The number of graphics frames is limited only by computer memory. When selected, frames can be created and resized in the graphic region with the mouse.

The Frame tool properties menu consists of:

Split Selected Frames	Divides graphics frames into specific number of graphics frames.
Delete	Deletes all graphics frames, all selected graphics frames, or all unselected graphics frames.
Clear	Clears all graphics frames, all selected graphics frames, or all unselected graphics frames.
Select All Frames	Selects all graphics frames.
Load Frame Layout	Loads graphics frames from a file in the `$CSIDIR/gframe` directory.
Save Frame Layout	Saves graphics frames into a file in the `$CSIDIR/gframe` directory.
Frame Color	Changes the frame color of graphics.

Zooming Tool

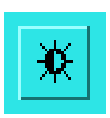


Currently not implemented for CSI (localized FID or MVS) data displays.

The Zooming tool selects a portion of an image or a spectrum to be expanded. Cursors are displayed on all currently selected Gframes. The cursors are XORed to the display. The Zooming tool properties menu consists of:

Zoom	Expands selected images.
Unzoom	Contracts selected images.
Bind	Adjusts the zoom lines to all selected images. Zoom lines are the lines that control the portion of images to be zoomed.
Cursor Tolerance	Controls cursor sensitivity for the zoom lines. This specifies how close the mouse cursor must be to a zoom line to select it.
Pixel Interpolation	Expands image size to display on screen. Used not only when zooming, but any time an image is redisplayed.

Vertical Scale Tool



The Vertical Scale tool adjusts the vertical scale of an image. When the Vertical Scale tool is active, frames cannot be selected or deselected with the mouse, because clicking on an image changes the displayed intensity instead. However, a frame does not have to be selected in order to adjust its vertical scale with the mouse; any image that is clicked on is rescaled.

Vertical scale can be adjusted two ways:

- Click the left mouse cursor on the image. The program finds the maximum data value within a ten-pixel square box centered on the cursor and the vertical scale is adjusted to put this pixel at the top of the grayscale.
- Use a window to enter the desired vertical scale value.

Figure 67 shows the Vs Prop (Vertical Scale Properties) menu for selecting vertical scaling

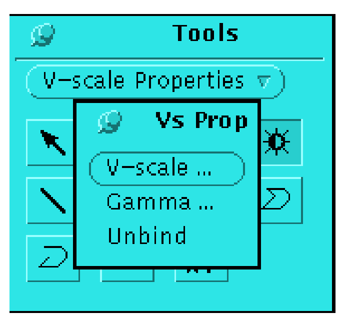


Figure 67. Vertical Scale Properties Window

(V-scale option), gamma correction (Gamma option), and binding or unbinding images. Each property is described in the following sections.

Vs Prop Menu: Vertical Scaling

The V-scale option of the Vs Prop menu displays the Vertical Scaling window in which vertical scaling can be set, as shown in Figure 68. The range of data values to be mapped to grayscale values and the form of the mapping function can both be changed. Any changes in vertical scaling are applied to all the selected Gframes. Changes to the mapping function are also applied to any new images when they are loaded, but the data range is scaled to match the data in the particular image.

The graph at the bottom of the Vertical Scaling window is a plot of gray level as a function of data value. (The "gray level" corresponds to the index into Image-Browser's colormap. The intensity of the screen pixel as a function of colormap index is set by the Gamma Correction window, discussed in "Vs Prop Menu: Gamma Correction" on page 151.)

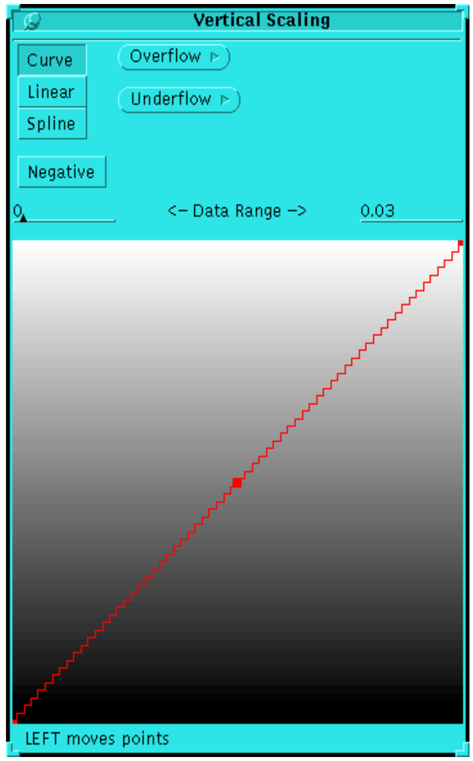


Figure 68. Vertical Scaling Window

Data Range

The range of data values to map to the full range of gray values is set by the two type-in fields labeled Data Range. The data values are plotted linearly along the horizontal axis, between the values in the Data Range fields. (The Return key must be pressed in at least one of the fields for the changes to take effect.)

Mapping Function

The shape of the mapping function is selected by the buttons at the upper-left of the Vertical Scaling window.

The mapping function translates the data value in a pixel to a corresponding grey level. In the following discussions, normalized variables are used: x and y, for the data, and for the grey level values, d and g. These variables are defined as

$$x = \frac{d - d_{min}}{d_{max} - d_{min}} \quad \text{[Eq. 27]}$$

and

$$y = \frac{g - g_{min}}{g_{max} - g_{min}} \quad \text{[Eq. 28]}$$

Therefore, both x and y vary from 0 to 1. Note that with the appropriate gamma correction (discussed in the next section), the actual screen intensity will vary exponentially with y.

For any type of mapping function, the Negative button can be selected to invert the intensity scale; that is, the minimum grey value will be white and the maximum, black.

Curve Mode

The type of mapping function is selected by the buttons at the upper-left of the Vertical Scaling window. The default is curve, which provides a flexible functional form that includes power functions and a close approximation to exponential functions. The two parameter family of curves are controlled by moving the curve's control point around with the left mouse button. The left and right ends of the line can also be moved up and down. The form of the function depends on which regions of the graph the control point is in.

If the control point is in region 1, as shown in the Figure 69, the following equation shows the defining function for these curves:

$$y = \left(\frac{x}{x - ax + a}\right)^b \qquad \text{[Eq. 29]}$$

where a and b are the two adjustable parameters. The ranges of a and b are:

$$a > 0,\ 1 \le b \le 10 \qquad \text{[Eq. 30]}$$

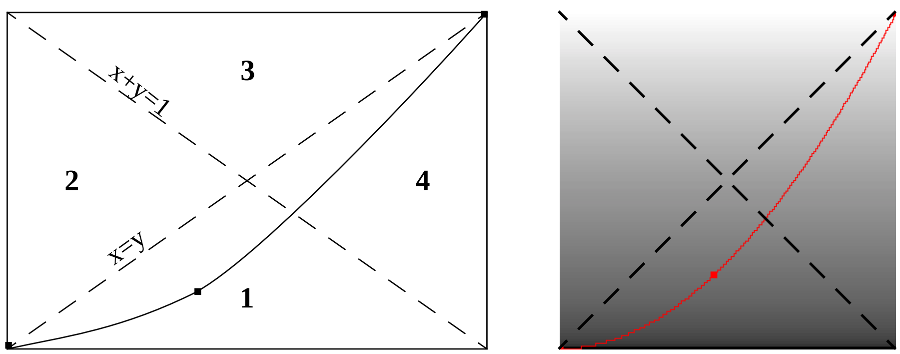


Figure 69. Curve Control Point

Note that if $a = 1$, this reduces to a power function, which is the case if the control point has $x = 0.5$. If the control point is in region 2, the curve is reflected through the $x = y$ line. This family of curves includes power functions of the form

$$y = x^{1/b} \qquad \text{[Eq. 31]}$$

which applies when the control point is on the $y = 0.5$ line. When the control point is in region 3 or 4, the curves for regions 2 or 1, respectively, are reflected through the $x + y = 1$ line.

Linear Mode

The linear mode allows the user to specify a piecewise linear function that passes through all of the control points. Any additional number of control points can be added by clicking the left mouse button anywhere on the canvas away from an existing control point. Control points can be deleted by clicking on them with the middle mouse button.

It is a good idea to avoid large discontinuities in the slope of this function at the control points. Due to the characteristics of human vision, these discontinuities can make a surface that increases smoothly in intensity across a picture appear to be non-monotonic in intensity! For this reason, the third mode might be more useful.

Spline Mode

The spline mode is like linear mode, except that a spline curve is drawn through the control points instead of straight lines. The spline mode is also coupled to the linear mode in that the two modes share the same control points; changing the control points in one mode also changes them in the other.

The spline function used here interpolates between control points with cubic polynomials, arranging that the slopes match at the control points. The final curve is continuous up to the second derivative. At the endpoints second derivative is forced to zero—the defining condition for the so-called “natural” cubic spline.

Underflow and Overflow

The Underflow and Overflow menus control how data values outside of the domain of the mapping function are displayed. The default is Off, meaning that data values less than the “minimum data value” ($x < d$) are displayed the same as $x = d$, and that data values $x > D$ are displayed the same as if $x = D$. The menus offer a number of alternative color choices for such values.

Vs Prop Menu: Gamma Correction

The Gamma choice in the Vertical Scaling Properties window opens the Gamma Correction window, shown in Figure 70.

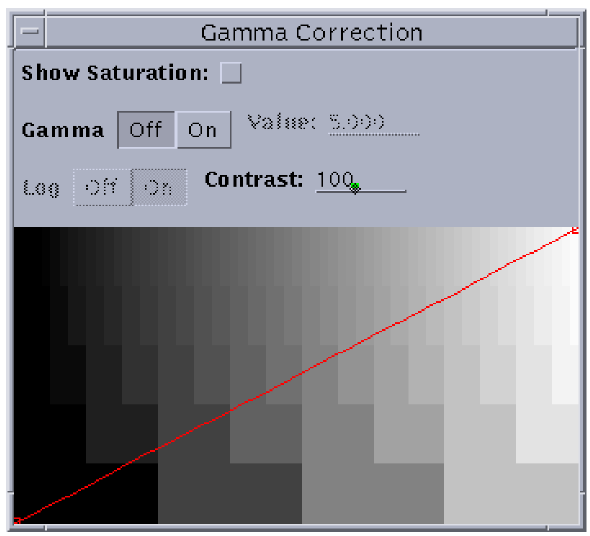


Figure 70. Gamma Correction Window

The primary purpose of gamma correction is to make optimal use of the limited number of grayscale steps in ImageBrowser’s colormap. A secondary purpose is to compensate for any unusual nonlinearities in the monitor’s displayed intensities. Compensation allows images to appear the same with identical scaling on any monitor—once gamma correction has been done. For a properly adjusted monitor, minimal gamma correction should be necessary.

Gamma Correction Window

The Gamma Correction window has a plot at the bottom that graphs the pixel value (between 0 and 255) against the index into the grayscale portion of ImageBrowser’s colormap. (Pixel value is actually a color that has a red, green, and blue value, but the grayscale always uses the same value for each color.) The graph background is painted with several rows of gray steps to demonstrate the current gamma correction. The top row shows every step in the grayscale ramp; the second row, every other step; the third row, every fourth step; and so on. (It appears to the eye that each ramp step is shaded from a lighter gray on the left to a darker gray on the right. This is an *optical illusion*, which can be seen by masking out the surroundings of one of the steps with a paper frame.)

Ideally, no steps should be visible anywhere in the top row, but, if the ImageBrowser colormap is fairly small (like the 64-step default for 8-bit color machines), they can be easily seen. The goal of gamma correction then becomes to make each intensity step equally apparent to the eye. For a short grayscale ramp, this process can involve looking only at the top row of steps. For a larger ramp, the second or third row might need to be examined. (The size of the grayscale ramp is set in the `colormap.init` file in the `$CSIDIR` directory. See "Initialization Directory," page 133, for details about CSI initialization.)

Adjusting the Monitor

Before adjusting the gamma correction, adjust the monitor. Some monitors have no easily accessible brightness control; therefore, monitor adjustment should be performed by a service person.The most common problem with monitor adjustment is that the black level is set too dark, making everything near the bottom end of the intensity scale appear black. Set the "brightness" control (labeled ☼ on some monitors) just low enough so that the blackest level, at the left of the grayscale ramps (pixel value 0), is indistinguishable from the unscanned black background at the edge of the monitor screen. To accomplish this adjustment, it might be convenient to move the Gamma Correction window slightly off the bottom of the screen, so that the bottom row of steps directly merges with the unscanned margin.

Once monitor brightness has been adjusted correctly, the perceived prominence of the intensity steps in the Gamma Correction window should be roughly equal with no gamma correction.

Gamma Correction

The gamma correction described in the following paragraph is still effective on a poorly adjusted monitor; although, if the brightness is set too high, there is no way that the lowest gray level can be made entirely black.

Two forms of gamma correction are available. When the Gamma and Log switches are both set to ON, ImageBrowser attempts to make each step in the colormap index an equal step in the log of the screen intensity, which assumes that the screen intensity is described by a function of the form:

$$I = I_0 + V^{\gamma} \qquad \text{[Eq. 32]}$$

where I is the intensity, V is the voltage (proportional to the pixel value) γ is a characteristic of the monitor (equal to about 2.5), and I_0 is the background intensity due to room illumination or poor adjustment of the monitor.

The Value field next to the Gamma switch controls the value of γ used in the above equation. The Contrast field, next to the Log switch, specifies the value of the ratio of maximum to minimum displayable intensities, in effect, I_0 in the previous equation. Normal values for a properly adjusted monitor are 50 to 100 for I_0 and about 2.5 for gamma. If the monitor brightness is not properly adjusted, it is still usually possible to get a good fit by adjusting γ; the function is relatively insensitive to the Contrast value.

When the Gamma switch is on, a "control point" is displayed near the middle of the gamma correction curve. This control point can be dragged with the left mouse button to adjust the Gamma value. The Contrast value can only be changed by typing a new value in the text field.

If the Gamma switch is ON and the Log switch is OFF, correction is made for equal steps in intensity, according to the formula $I = V^{\gamma}$

This correction is not ideal, but it might be useful for emphasizing the contrast in some region of the colormap, which could normally be done with the V-scale function instead.

Vs Prop Menu: Unbind or Bind

The last choice in the Vertical Scaling Properties menu is Bind or Unbind:

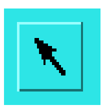
- If Unbind is displayed, the current mode is bound, and the new VS value is applied to all selected images, as well as the one clicked on.
- If Bind is displayed, it means that the current mode is unbound. When an image is clicked on, only that image is rescaled.

The Bind mode has no effect on the operation of the Vertical Scaling window because values entered there always are applied to all selected frames.

ROI Tools

This section describes the functions of graphics tools for selecting, drawing, marking, annotating text, phasing and scaling spectra, and selecting voxels on graphic regions of interest (ROI).

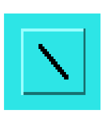
ROI Selector Tool



The ROI Selector tool selects and adjusts any of the regions of interest. This tool is the default mode of the graphics tools. After any ROI has been drawn, the ROI Selector tool becomes active. The tool has the following ROI Properties menu (as do all the ROI tools).

Delete	Deletes ROI.
Load	Loads ROI tools from a file in the `$CSIDIR/roi` directory.
Save	Saves ROI tools to a file in the `$CSIDIR/roi` directory.
Color	Changes the ROI tool color. The colors of all the ROIs and labels are changed.
Font Size	Sets the size to use for the next annotation entered. The size cannot be changed after the label has been created. Choices are 10 pt., 12 pt., 14 pt., and 19 pt.
Cursor Tolerance	Adjusts the sensitivity of the cursor. This is how close the mouse cursor must be to an ROI vertex to select that vertex.
Bind/Unbind	Bind and unbinds current mode.

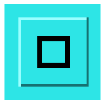
Line ROI Tool



The Line ROI tool draws a line ROI. This tool is used in the Line Data processing function.

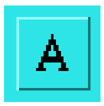
It is also possible to obtain statistics from a line ROI; although, this might not generally be useful. The points included in the statistics are the points along the line. To draw a line after the tool is selected, position the cursor at one of the desired endpoints, press the left mouse button, and drag the cursor to the other end point. As the cursor is being dragged, an XORed line is drawn. Release the left mouse button, and the line appears in the selected ROI color.

Box ROI Tool



The Box ROI tool draws a rectangular ROI. It is used in the statistics processing function. To draw a rectangular ROI after the tool is selected, position the cursor at one of the desired corner coordinates, press the left mouse button and drag the cursor over the desired region of interest area. As the cursor is being dragged, an XORed rectangle is drawn. When the left mouse button is released, the completed rectangle appears in the selected ROI color.

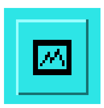
Annotation Tool



The Annotation tool annotates text. After it has been selected, position the cursor at the desired spot and click the left mouse button. An underscore cursor appears at the marked location, indicating that the label is selected and ready to accept typed input.

Typed characters are always added to the end of the annotation field; characters cannot be inserted into the middle of a string. The label can be selected and moved to other locations at any time. If more than one label is selected, any typed input is appended to all of the selected labels.

Spectrum Tool

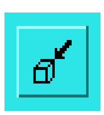


The Spectrum tool is used for manual phasing and vertical scaling of a spectrum. After a spectrum has been selected by the Voxel Select tool, this tool can be selected to do phasing and scaling. The Marker Properties menu contains phase adjustment types.

To phase a spectrum, place the cursor on the selected spectrum and drag the left mouse button. Scaling is done with the middle mouse button. When the middle mouse button is clicked, the spectrum scale is proportionately increased or decreased depending on the distance of the cursor from the baseline origin of the spectrum.

If the cursor is placed at the left-hand side of the spectrum, click the middle mouse button to move the origin of the spectrum to the location of the cursor (Const&Linear phasing is not currently implemented).

Voxel Select Tool



The Voxel Select tool allows a very quick way to look at selected spectra within a CSI data set. This tool can be used on localized FID data, MVS data, or curve fit MVS data.This tool allows a voxel to be selected out of a CSI grid and displayed in its own frame.

After it has been activated, when a Gframe is selected without CSI data displayed in it, the frame is selected. When CSI data is displayed in the Gframe, the voxel (that the cursor is in when the left mouse button is clicked) is copied into the selected Gframe. If more than one Gframe has been selected, an error results.

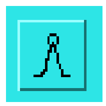
To scale the selected spectrum, select the View option from the command panel. Select Display Properties. In the Display Control window, choose Auto, Normalized, or Fixed scaling. Select an axis to be displayed in Hz or ppm. (*axis is not yet implemented*).

This tool can be used in conjunction with the processing functions when selecting individual spectrum for processing.

Marker Tools

This section describes the functions of graphics tools for marking points on spectra and spectra data, and tools for curve fitting and voxel shifting.

Picking Tool



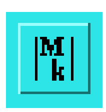
The Picking tool allows points to be marked on a spectrum for peak and baseline processing. It is used in the baseline correction and curve-fitting processing functions.

To mark a point after the tool is selected, position the cursor at the desired point and click the left mouse button. A marker appears and is selected. Whenever this function is used, the Edit OK option must be selected afterwards in order for these user-defined points to be put into the peak or baseline lists.

The properties menus of the Picking tool consists of the following:

Delete	Deletes all selected points.
Frequency Difference	Display the frequency difference between two points, and the frequency at a specific point.
Move Axis Origin	Moves the origin of the axis.
Color	Changes the tool color.
Aperture	Adjusts the sensitivity of the cursor. Cursor sensitivity determines how close the mouse cursor must be to a marker to select that marker.

Vertical Line Marker Tool

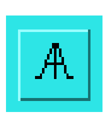


The Vertical Line Marker tool allows specific locations to be marked in the data and is used only on spectra data in the CSI tool. Use this tool to display the frequency difference between two points, and the frequency at a specific point.

The Vertical Line Marker tool is also used to remove unwanted peaks in a spectrum. Use the Baseline Correction process to remove peaks. After a Spline or Polynomial baseline correction has been specified, mark a region with two points. Select the rm Peak option to perform the correction and fill in the data between the two points with the baseline correction data.

The properties menu of the Vertical Line Marker tool is the same as for the Picking tool.

Curve Fitting Tool



The Curve Fitting tool displays a cross-hair (+) cursor. This tool is used for interactive curve fitting. When clicked, the height and width of the desired curve can be adjusted by selecting the endpoints of the cross-hairs with the cursor and dragging the ends to their desired length.

Filtering Tool

This section describes the weighting and filtering tool.

Weighting and Filtering Tool

The Weighting and Filtering tool allows weighting functions to be interactively set and applied to individually selected spectra. This tool is used in conjunction with the spatial and spectral reconstruction processes.

When the Weighting and Filtering tool is selected, three windows open in the selected frame. The top window contains the transformed data; the middle, the filtering (weighting) function; and the bottom, the untransformed data. Use the mouse buttons to control the shape and position of the filtering functions.

SELECT (in the weighting function window)	Adjusts the Time Const. field.
ADJUST (in the weighting function window)	Adjusts the Shift Const. field.

This tool works on two types of data:

- *Raw Data (Spatial Filtering)* – If no data exists in the currently selected frame, spatial filtering is selected when the tool is entered. The spatial filtering tool is quite limited regarding the data that is used. Only the voxels making up the midpoint of the data in the *x* (fast) direction are selected. After data has been selected, filtering functions in the Spatial Reconstruction window (Point f1, Filter Type, Time Const., Shift Const., Delay) can all be interactively selected to adjust the filter applied to the data.
- *Localized FID Data (Spectral Filtering)* – For processing localized FID data into spectral data, a spectrum must exist in the selected graphics frame. This is the default selection if a spectrum does exist in the frame. After data has been selected, filtering functions in the Spectral Reconstruction window (Matrix, Filter Type, Time Const., Shift Const.) can all be interactively selected to adjust the filter applied to the data.

6.4 Processing Functions

When an entire CSI data set is being processed, the interaction is different than when a selected voxel is processed. When applying an operation to the whole CSI data set, the data might not necessarily be displayed. The CSI tool has the following global data buffers for CSI data:

- CSI raw data
- Localized FID data
- Multivoxel spectra (MVS)
- MVS curve-fitted data
- Metabolic map data

The CSI tool has the following global data buffers for reference image data:

- Raw image data
- Reconstructed image data

Most processing operations on an entire data set operate on one global data buffer and process it into another global data buffer. These global data buffers keep their data until another processing operation is performed that overwrites the data buffer. That is, even though MVS data is being processed and displayed, the processing operation to transform raw data into localized FID data can be run at any time. Also, when performing a processing

operation on the entire data set, one and *no more than one* graphics frame must be selected. This selected graphics frame is the destination used to display the data after the processing operation has completed.

Data interaction is different when processing individual spectra. Individual spectra are usually selected and processed before performing a global operation in order to set up the processing attributes to use on the entire data set. The currently selected frame should hold the desired spectrum to be processed. Spectra can be inserted into this frame by using the Voxel Select tool, described on page 154, or by selecting the voxel with the current processing window. When processed, the spectrum is stored back to the currently selected frame.

Select processing functions from the Process option in the CSI command panel with the right mouse button. Click Process with the left mouse button to activate the current default process. The current default process starts at Spatial Reconstruction and is incremented after each option until the Metabolic Map process.

Spatial Reconstruction

The spatial reconstruction process performs a 1D or 2D transform along the spatial axes on the CSI Raw data set to form the localized FID data set. The size of the spatial axes is the default Matrix size. The Matrix field can then be expanded to provide for zero-filling. Figure 71 shows the window for the spatial reconstruction process.

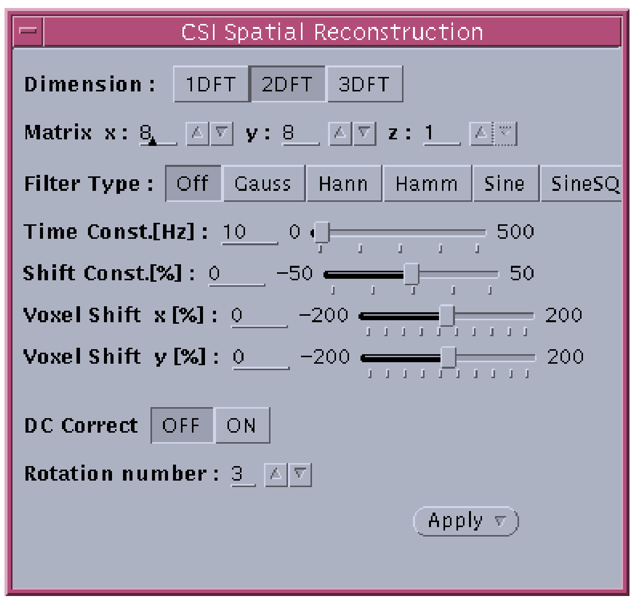


Figure 71. Spatial Reconstruction Window

The following list describes the functions of the spatial reconstruction processing attributes.

Dimension	Defines the spatial dimensions of the data set 1D or 2D.
Matrix	Defines the size of the spatial dimensions.
Filter Type	Selects a weighting function if desired to be applied to the data.
Time Const	Used with Filter Type to fit the weighting function to the data.
Shift Const	Used with Filter Type to fit the weighting function to the data.
Voxel Shift	Spatially shifts the voxels in both directions.

DC Correct	Applies dc correction to the data.
Rotation number	Rotates the fields in 90° increments. The default is a rotation of 3, which aligns fields for VNMR reference image data.
Apply	Transforms all the voxels by using the selected modifications.

Interactive Filtering or Weighting

Interactive filtering can be performed with this operation in order to determine the best function and filter parameters. As the filtering function is adjusted, the Time Constant and Shift Constant sliders move to the adjusted values.

Spectral Reconstruction

Performs a 1D Fast Fourier Transform (FFT) on the FID in each voxel of the localized FID data set to form the multivoxel spectra (MVS) data set. Figure 72 shows the window.

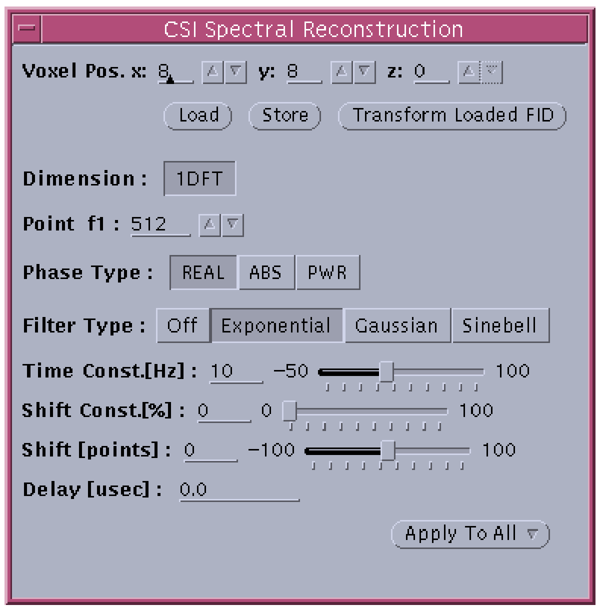


Figure 72. Spectral Reconstruction Window

The following list describes the functions of the spectral reconstruction processing attributes:

Voxel Pos	Uses values in this field, and the Load, Store, and Transform Loaded FID options, to allow changing one voxel at a time.
Dimension	Defines the spatial dimensions of the data set 1D, 2D, and 3D (3D is currently not supported).
Point f1	Defines the size of the spectral dimension. The number of points comes up as the default value but the value can be changed for zero-filling.
Phase Type	Defines whether the data will be processed as phase-sensitive data (REAL) or amplitude data (ABS).
Filter Type	Selects a weighting function if desired to be applied to the data: Exponential, Gaussian, Sinebell (not supported at this time)

Time Const	Used with Filter Type to fit the weighting function to the data.
Shift Const	Used with Filter Type to fit the weighting function to the data.
Shift (points)	Shifts data left or right by points. A positive number shifts data to the right; a negative number shifts data to the left.
Delay (µs)	Reflects the time, in µs, of the left or right data shift performed by the Shift function. Positive and negative delays corresponds to positive and negative shifts.
Apply To All	Transforms all the voxels by using the selected modifications.

Interactive Filtering or Weighting

Perform the following steps to apply a weighting function to a localized FID and interactively manipulate it to see the effect on the resultant spectrum in a selected Gframe:

1. Copy a FID into a selected Gframe by using the Voxel Select tool or by using the Voxel Pos. field and the Load option in the Spectral Reconstruction window.
2. Select the Filtering tool from the G-Tools window to open a Filter display in the selected Gframe.

After the filtering application is done, the processing features in the Spectral Reconstruction window can be used along with the left and middle mouse buttons to manipulate the filter. Clicking the left and middle mouse buttons within the weighting function display manipulates the values of the Time Const. and Shift Const. fields and displays the resulting spectrum. Changing fields within the window also updates the resulting spectrum.

Other spectra can be selected and processed by using the Voxel Pos. field and the Load option. However, selecting spectra by using the Voxel Select tool disables the Filtering tool until it is reselected.

Phase and Baseline Correction

Phase Correction and Baseline Correction corrects MVS data. This process is selected after spectral reconstruction if phase or baseline correction are needed for the data.

Figure 59 (page 141) and Figure 60 show the Phase Correction and Baseline Correction windows, respectively, that open when those options are selected from the Process menu. The processes allow for correction of a single voxel at a time or global correction of all the voxels. Individual spectrum can be phased or baseline corrected. Correction is done for both processes by selecting the spectrum with the Voxel Pos. and the Load option or with the Voxel Select tool. After phase or baseline correction (or both) is done for the individual spectrum, click the Store option to put the spectrum with the rest of the data. Click the OK option in each section to save phase and baseline coefficients. These saved coefficients can then be applied to all the voxels by using the Write all mode in the Global Phase Correction & Global Baseline Correction section in the Baseline Correction window.

For the Global Correction, a subset of voxels can be selected by using the Box ROI tool. After this tool is selected, the cursor can be positioned on the left-hand corner of a selected group of voxels. As the cursor is dragged across the screen, a rectangular field opens up and any voxels within it are selected when a global phase and baseline correction is requested. Only a portion of the voxel need be in the region for it to be selected.

Phase Correction

Local Phase Correction corrects a voxel spectrum in a selected Gframe loaded by the Voxel Pos. and the Load option. The voxel can also be selected with the Voxel Select tool. Click the Auto Go option to initiate the phasing. The OK option is used to store a set of phase coefficients.

Using Phase Correction

Phasing can be done on individual voxels or globally on all the voxels. To see how the autophasing or certain phase values will work, try it on a selected voxel spectrum. Anything done locally does not affect the data in the MVS data until you select the Store button.

Select the desired Phase Order and Auto Go to perform automatic phase correction on a spectrum in a selected Gframe.

Select the Spectrum tool to perform manual phasing. After the tool is selected, click on the voxel to phase. For more information, see "Spectrum Tool," page 154, and "Adjusting the Phase with the Spectrum Tool," page 142.

If the phasing results are satisfactory, select the OK option to save the phase values to be used with the Write all global phase mode.

The following list describes the functions of the Local Phase Correction processing attributes, shown in Figure 59.

Phase Order	Selects the type of Phase Correction: Constant, Linear, or Both.
Auto Go	Selects Automatic phasing.
Set rp	Sets the `rp` field to 180°or clears the field.
Set lp	Sets the `lp` field to Marker, -Marker, np(echo), or clear
	Marker searches for a line marker in a currently selected gframe and sets the `lp` value to 360**n*, where *n* is the nth complex data point specified by the Line Marker location. This option is useful for phasing an echo. To use Marker, do the following steps: 1. Voxel select a localized fid corresponding to spectra for phasing. 2. Put a Line Marker in the middle of the echo and press Marker. 3. Select gframe that the desired spectrum is in and apply `lp` phase
	-Marker is same as Marker except it sets a negative 360*n degree value.
	np(echo) sets `lp` to 180*`np`/2. Also used for setting `lp` for full echoes.
	Clear erases the contents in the `lp` field.
rp and lp	Fields that display the last applied values or the values to apply to the selected spectrum. rp and lp have the options Apply and Zero:
	Apply assigns the values to the spectrum in the currently selected gframe.
	Zero zeroes out the applied phases to the currently selected gframe.
OK	Saves the phase coefficients for future use.

Click on the Auto Go option to initiate phasing. The OK option is used to store the local rp and lp phase coefficients into the Global rp and lp phase correction, depending on the Phase order selection:

- If Const. is selected, the rp value is stored.
- If Linear is selected the lp value is stored.

- If Both is selected, both values is stored.

Global Phase Correction corrects all voxels selected by the Voxel Pos. and the Load option.

`rp` and `lp`	Fields that display the current values for Global Phase Correction.
Mode	Selects Write all or Automatic phasing.

To register the correction values for the Write all mode, select the OK button after the sampled points and the correction method are satisfactory, then select Apply To All.

Baseline Correction

Local Baseline Correction performs baseline correction on a loaded spectrum. Once again, the spectrum can be loaded with the Voxel Select tool.

Using Baseline Correction

Baseline correction can be performed by using sampled peaks or baselines. The SINC correction method works with peaks, and the Spline and Polynomial fitting methods work with baseline points.

To start sampling for the baseline correction:

1. Define the selection parameters, then click the Sampling Go option.
2. After the initial sampling points have been placed on the spectrum, use the Picking tool to augment baseline or peak points that have been missed.
3. After the display points are satisfactory, select Edit OK to save the displayed points for performing the correction.
4. If the correction is satisfactory, select the Correction OK option to save the correction values to be used with the Write all global correction mode.

To globally remove peaks on all the voxels (or the selected voxels by using the Box ROI):

1. Select the Correction OK option.
2. Select the rm Peak item, the Write all mode, and the Apply to All option.

The following list describes the functions of the baseline correction processing attributes.

Sampling Item	Selects Baseline or Peak. Baseline sampling usually needs to be augmented by using the Picking tool.
Sampling Points	Sets number. It must be in the range of 10 to 20.
Prior Knowledge	Used with the Peak File (PK File) for peak sampling.
PK File	List Prior Knowledge peak files stored in the `$CSIDIR/PEAK` directory.
Sampling Phase	Indicates which part of the complex data to sample: Real, Imaginary, or Both.
Correction Method	Selects spline, polynomial, or SINC. Spline and Polynomial are used after baseline sampling has been done. SINC is used when peak sampling has been done.
Polynomial Order	Sets the order for polynomial correction.
Correction Go	Performs the selected correction on the data.
Correction OK	Saves correction values for use with global Write all correction.

Global Baseline Correction is done by ensuring that Item and Mode are correct and clicking the Apply option. Use the Box ROI tool to select a subset of the total number of voxels.

Mode	Set to Write all or Automatic. Write all uses the last set of local phase or baseline corrections and applies it to all the spectra. Automatic does everything automatically.

Metabolic Map Calculation

Metabolic Map (Mmap) Calculation performs the curve fitting and peak picking necessary to create a metabolic map. After peaks have been selected and fitted, metabolic maps of selected peaks can be made. See Figure 61 for the Mmap Calculation window, which contains curve fitting.

Mmap calculation and curve fitting works the same way phase and baseline correction works. It is best to select a spectrum, perform local peak picking and curve fitting on the local spectrum, and then perform global curve fitting.

The following sections describe the functions of Mmap calculation processing attributes.

Local Peak Picking

Local Peak Picking is performed the same way as for the Peak Sampling mode in baseline correction. It works on a selected spectrum in a selected Gframe. One, *and only one*, Gframe can be selected. The following list describes the functions of the attributes that appear in the Local Peak Picking portion of the Mmap calculation window.

- Sampling Mode (Manual, Automatic). If Manual is selected, use the Picking tool; otherwise, select Automatic.
- Prior Knowledge. If Use is selected, the correct PK File must be selected.
- PK File selects a set of predefined peaks. These files are located in the CSI initialization directory under PEAK. Standard files have been set up, but additional peak files can be defined the user.
- Sampling Go finds the peaks in the spectrum and displays markers at each peak.
- Edit OK registers the peak information from the picking markers in the selected spectrum. These markers might have be added, moved, or deleted after the Sampling Go process was performed.

To perform automatic peak picking:

1. Click the Sampling Go option.
2. Load a voxel spectrum into a selected Gframe.
3. Use the Picking tool to modify selected peaks, and then click Edit OK to register these peaks.

   Alternatively, desired peaks can be selected by using the Picking tool without using any automatic peak picking.

Peaks must be selected for the curve-fitting routines to work.

Local Specification

Local Specification is required to start with the manual mode to register the peaks and metabolic map information. Click on Specify CurveFit and Mmap to open the Interactive Fitting Tool window shown in Figure 73; you must have MVS data to open this window.

The following list describes the functions of the attributes that appear in the Local Specification portion of the Mmap calculation window.

- Item (Specific,Total Spectrum) fits either one line at a time or the entire spectrum.
- Curve Type (Gauss Lornz, SINC Lrnz, Const S.L.) selects the type of line shape to fit.

Interactive Fitting Tool

The Interactive Fitting Tool allows peaks and curve fits to be checked, curve-fits to be adjusted, and peaks and curve-fits to be registered. A frame with a voxel spectrum must be selected before this tool can be activated.

To register the peaks and metabolic maps, this tool must be activated when initially processing data. After this information is registered, it can be used to process other data sets. The tool need not be activated again until curve-fitting or map information is to be changed. Select Fitting Go in the Manual mode to activate this tool.

The Interactive Fitting Tool window, shown in Figure 73, allows curves for each peak to be viewed, curve parameters to be changed, metabolite names to be assigned, and numbers to be mapped.

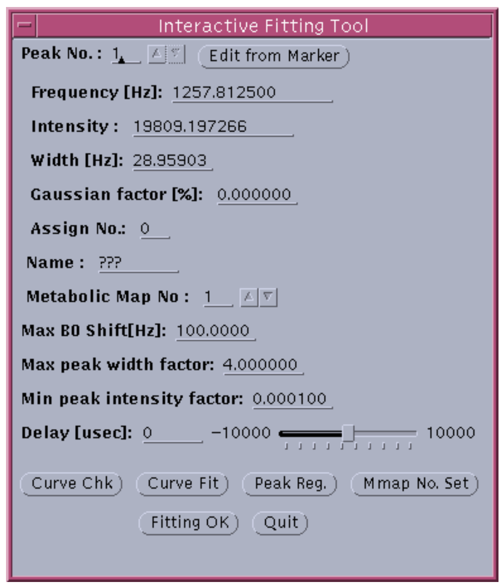


Figure 73. Interactive Fitting Tool Window

Curve Check displays a curve fit on the selected peak or on the total spectrum, depending on which item was selected in the Interactive Fitting Tool window. Curve Check uses the displayed parameters to draw the curve. Auto Curve Fit performs a curve fit on the selected spectrum.

Click Peak Reg. to register all the peaks if the peak values are satisfactory. Use Mmap No. Set to register the peaks desired for metabolic maps. Peaks are selected by assigning a number in the Metabolic Map No. area. The value 0 deselects that peak. Fitting OK registers the fitting parameters for the defined peaks. These options only need to be selected when the local curve fit is satisfactory.

The following list describes the functions of the processing attributes that appear in the Interactive Fitting Tool window. The attributes Peak No., Edit from Marker, Gaussian Factor, Assign No., Name, and Metabolic Map No. are peak specific.

Peak No.	Assigns a number to the current peak being fitted. Fitted curve is automatically displayed over spectrum. Frequency, Intensity, and Width are fields associated with this peak.
Edit from Marker	Updates and displays Peak No. and associated fields with peak and information from selected cross-hair markers.
Gaussian Factor	Assigns curve-fitting factor.

Assign No.	Assigns a number to a peak. Used with the Prior Knowledge file specified in the Mmap calculation window, shown in Figure 61. Zero means unused.
Name	Assigns a name (a character string) to a peak.
Metabolic Map No.	Assigns a map number.
Max B0 Shift	Specifies the maximum frequency shift difference that a peak can have from its defined frequency when generating a Mmap.
Max Peak Width Factor	Specifies the maximum width a peak can have from its defined value when generating a Mmap.
Min Peak Intensity Factor	Specifies the minimum peak intensity that a peak can have from its defined value when generating a Mmap.
Delay	Assigns a delay when performing spectral reconstruction.
Curve Check	Redisplays the fitted curve.
Peak Registration	Registers all peaks as confirmed information. Done for all peaks, not just the displayed peak.
Mmap No. Set	Registers all metabolic map numbers with their peaks. Done for all peaks, not just the displayed one.
Auto Curve Fit	Curve fits all peaks. Overlays curve fit on selected spectrum.
Fitting OK	Assigns local fitting parameters to global ones to help the global curve fit routines and closes the Interactive Fitting Tool.
Quit	Exits from the Interactive Fitting Tool window.

Metabolic Map Display

After performing peak picking and curve fitting, select the desired peaks, and click on Display Mmap to open the Metabolic Map Display window shown in Figure 74.

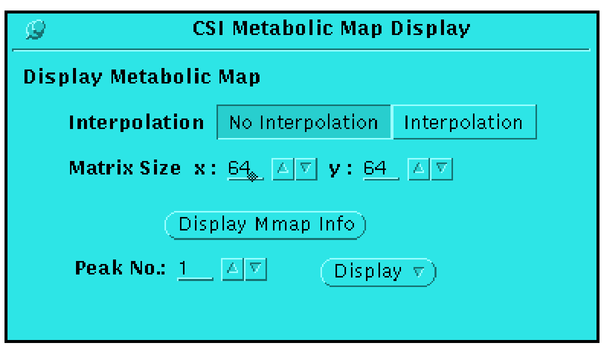


Figure 74. Metabolic Map Display Window

Processing Attributes

The following list describes the functions of Metabolic Map Display processing attributes.

Interpolation	Selects No Interpolation or Interpolation: No Interpolation displays a metabolic map grayscale image of the voxels in the MVS data set. Interpolation allows a selection of the matrix size greater than the number of voxels in the MVS data set, and it interpolates between the different intensities.
Matrix Size	Number of discrete voxels to use metabolic map display.
Peak No.	Peak number to form a metabolic map.
Display	Take selected peak and display its map.

Image Reconstruction

The Image Reconstruction window, shown in Figure 75, transforms a standard 2D field of view reference image.

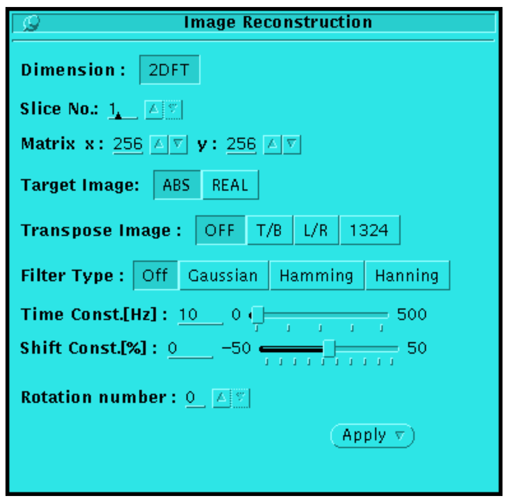


Figure 75. Image Reconstruction Window

Processing Attributes

The following list describes the processing attributes in the Image Reconstruction window.

Filter Types	Weighting functions applicable to the raw data. (Not implemented)
Time Const	Property of the weighting functions that can adjust the functions to the data.
Shift Const	Property of the weighting functions that can adjust the functions to the data.
Rotation number	Allows rotating images in 90° increments.

The raw data can also be transposed by using the Transposed Image selections before transforming. The matrix values are selected by the number of points in the data file, but can be adjusted to allow for zero-filling.

It is generally easier and better to read in the images. In the future, Image Reconstruction may be made obsolete as a processing function.

Metabolic Image Calctool

The metabolic Image Calctool is a calculation tool for spectral peaks from the MVS data. It can add, subtract, multiply, and divide peaks. Set the result equal to a new value to create new peaks. Click Save to save the created peak to the metabolic map data buffer.

Figure 64 on page 146 shows the Image Calctool and an example calculation. The calculation adds peaks 1 and 2 together and multiplies them by a constant 2.0. Peaks are specified by integers, constants are specified by real numbers. A peak number might or might not be specified as a result. In this example, a peak number is specified as a result. To execute this calculation, click on the  button.

Even though a peak number has been specified as the result, the storage of this calculation is not performed until the Save option is selected. If no peak has been specified in the result, a peak (map) number can be entered in the Save Check window, shown in Figure 65 on page 146. Select Save to activate this window.

pH Map Control

The pH Map process can create pH maps or frequency difference maps. pH maps are generated with the calculation:

$$\text{ph} = \text{pK2} - ln[(s-b)\ \S\ (a-s)]$$

where s is the chemical shift difference between Pi and PCr; and a, b, pK2 are constants.

In the pH map processing function, the correct peaks must be specified. The constants are set to default values but can be changed.

Figure 76 shows the window for the pH map process.

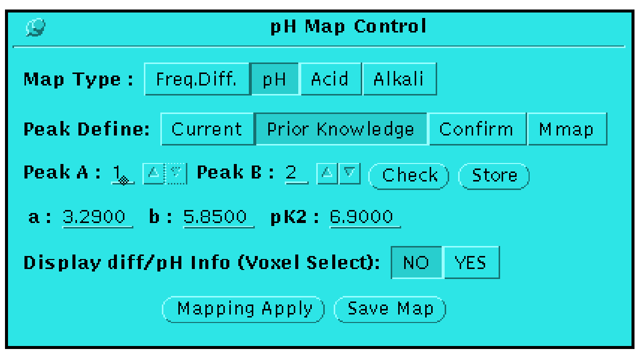


Figure 76. pH Map Control Window

The pH map process can also generate frequency difference maps between any peaks in the CSI spectra and acid and alkali variations of the pH map.

The box ROI can be used to select a region of interest when applying a global map by using the Prior Knowledge or Confirm Peak definitions.

The following list describes the functions of pH Map Control processing attributes.

Map Type	Type of map to generate: Freq. Diff., pH, Acid, or Alkali
Peak Define	Source of information to define the peaks: Current, Prior Knowledge, Confirm, or Mmap.
	Current is for a selected spectrum, cannot be used for global apply.

	Prior Knowledge and Confirm use previously registered prior knowledge or confirmed peak picking information with the MVS data buffer to determine the peaks for a local or global mapping. Mmap uses already curve-fitted metabolic map information to determine the peaks for a local or global mapping.
Peak A, B	Peaks in spectrum to obtain the difference in frequency.
Check	Performs a check of the frequency difference or pH in currently selected spectrum and displays result in the Info Message window.
Store	Saves the frequency difference in the current voxel-to-global map.
Display diff/pH info	Selects whether or not to output diff/pH values to Info Message window when performing global mapping.
Mapping Apply	Performs global mapping of Map Type by using Peak Define and displays map in currently selected Gframe.
Save Map	opens a Save Check window that is the same type window as the Image Calctool save window. It allows the mapped image definition to be saved into the current global buffer of mapped images. The window opens with metabolic map number set to 1 plus the number of global metabolic maps.

ROI Spectrum

ROI Spectrum is used with the ROI Line tool and the ROI Box tool on reference images:

- Used with the ROI line spectrum, it extracts and stacked plot of all the spectra underneath the ROI.
- Used with the ROI Box tool, it extracts and average spectrum of all the spectrum within the box. It relates areas in a reference image to the voxel spectra in its CSI data set.

To generate a stacked plot of spectra, use the ROI Line tool to draw a line across a reference image. Then, select ROI Spectrum from the Process menu, and a series of stacked spectra appear in one of the canvas windows.

To generate an average of all the spectra in an ROI region, use the ROI Box tool to draw a box in the desired region of a reference image. Then, select ROI Spectrum from the Process menu, and an averaged spectrum appears in one of the canvas windows.

6.5 Files and Other Items

This section describes file input and output and the error and information displays.

FileBrowser

The FileBrowser is a standard interface used for storing and retrieving files. It is always used when saving files. It is also always used when retrieving image files.

The Gframe, ROI, and Filter interfaces use the FileBrowser for saving files but do not use it for retrieving files, because the Load interfaces are built for quick access and always assume a specified directory. For more information about the particular directory for these interfaces, see “Tools,” page 147.

Figure 77 is an example of a FileBrowser window for loading images. The basic window is the same for most operations. The title of the window (in this case, FileBrowser: Data) describes the use of the current File-Browser window. In the case of loading movie images, the title is Movie Frame Loader; for ROIs, it is FileBrowser: ROI. When files are saved, Load is replaced by Save. Load All does not change because there is no corre-sponding Save All command.

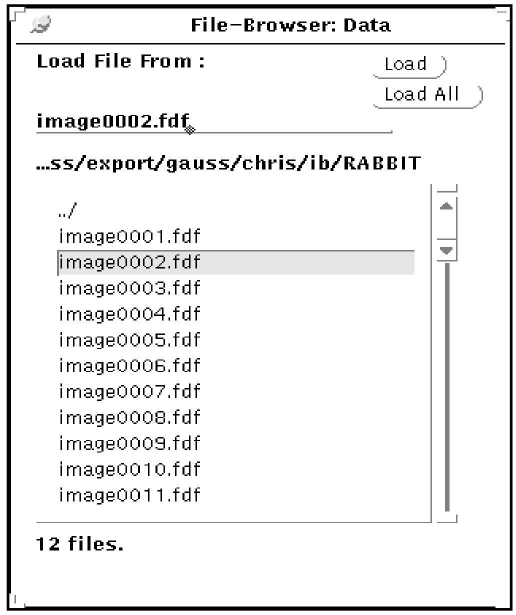


Figure 77. FileBrowser Window

The FileBrowser displays the currently selected file on the top line. Just below that is the current directory. The number of files in the directory is listed at the bottom. There is a scrolling window that contains the names of all the files in the directory. Subdirectories are indicated with a "/" at the end of their name. To select a name in the scrolling list, position the cursor over the desired name and click the left mouse button.

Changing Directories

Change directories by either double clicking on the directory name with the left mouse button, by selecting the name so it appears in the top line and pressing the Return key, or by entering the name directly in the top line and pressing the Return key. Note that the UNIX prefix "~" works in the FileBrowser. The "`../`" entry opens the parent directory.

Loading Files

Select File from the command panel, then select Load to open a FileBrowser for loading files. To load a file into Image Browser, select the desired file and press the Load option. The file is loaded into the next available graphics frame. To select a particular frame to load an image into, immediately click on that frame before clicking the Load option.

To load all the files in the current directory, click the Load All option.

Select the FDF file and click the Load option to load FDF files. For VNMR phasefiles, the directory that contains the phasefile must be selected when the Load option is clicked.

Saving Files

Select the File, then Save to open a FileBrowser tool for saving files.

CSI saves data from the global buffers except for spectrum data, which it saves from the currently selected Gframe. Because data is saved from the Gframe, when a file name is entered or selected into the top line of the FileBrowser, and Save is clicked, a Save Tool window opens.

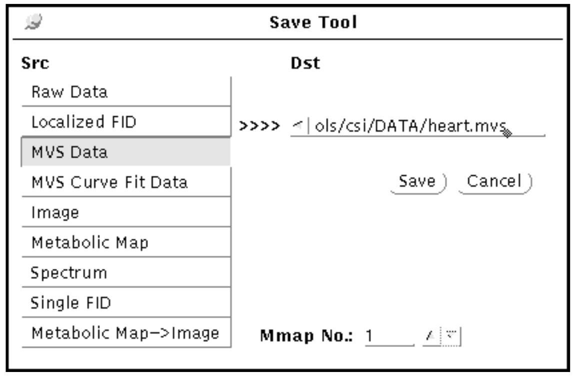


Figure 78. FileBrowser Save Tool Window

Figure 78 shows an example of a Save Tool window. The file name can be changed after the window has appeared.

The type of data to be saved must be selected. If Spectrum or Single FID is selected, the data must be in a selected Gframe.

If Metabolic Map->Image is selected, the appropriate metabolic map number must also be selected. A metabolic map is created and saved to the specified file. The metabolic map is created with the Matrix Size and Interpolation as specified in the CSI Metabolic Map Display window. For the Matrix Size and Interpolation to be set, a metabolic map must be displayed after the desired fields are selected; otherwise, the FileBrowser saves the metabolic map according to the specifications of the last displayed metabolic map.

View Menu

The following subsections describe the CSI, Image, Image/MV, MVSI Image, and Colormap options listed in the View menu on the CSI main command panel, shown in Figure 54 on page 135.

CSI Option

The CSI option displays one of the following global CSI buffers in the currently selected graphics frame:

- MVS data
- Localized FID data
- Raw data
- MVS curve fit data

Image Option

The Image option displays a global image buffer in the currently selected graphics frame:

- Reference image data
- Metabolic map image data

Image/MVS Option

The Image/MVS option displays the global reference image buffer overlaid on one of the following global CSI buffers in the currently selected graphics frame:

- MVS data
- MVS curve fit data
- Localized FID data

Image/MVS can be used for obtaining ROI Spectrum information by using the reference image.

MVS/ Image Option

The MVSI Image option displays one of the following global CSI buffers overlaid on a global reference image buffer in the currently selected graphics frame:

- MVS data
- MVS curve fit data
- Localized FID data

Colormap Option

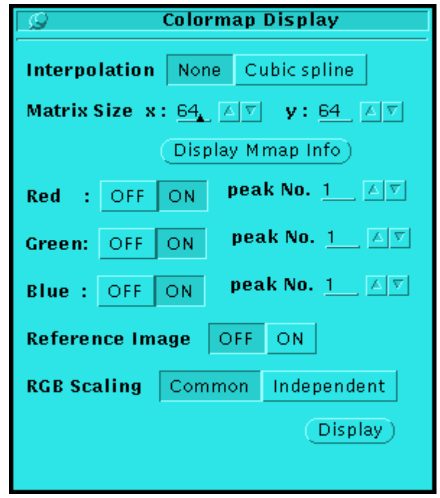


Figure 79. Colormap Display Window

The Colormap option opens the Colormap Display window, shown in Figure 79, to create color metabolic maps and overlays. Up to three different peaks can be displayed at a time and assigned to red, green, or blue colors. Interpolation can be performed between voxels to achieve a more continuous image.

Color maps overlaid on the current reference image can also be displayed. The intensities for each map can be independently scaled or scaled in common.

The Display Mmap Info option writes out a list of currently registered maps to the Info Messages window.

Display Properties

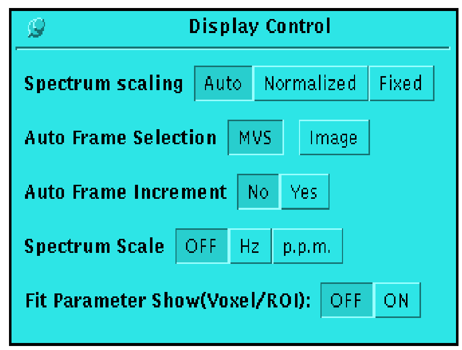


Figure 80. Display Control Window

CSI allows certain display properties to be selected. Figure 80 shows the Display Control window.

The following list describes the processing attributes in the Display Control window.

Spectrum Scaling — Controls how the spectrum is scaled when it is displayed in its own Gframe Auto, Normalized, or Fixed:

Auto scales each spectrum individually to the Gframe. This allows the full range of the spectrum to be seen, but it does not give a perspective to the rest of the voxels.

Normalized scaling normalizes the scale across the CSI data set and displays each spectrum in proportion to the other spectra in the data set.

Fixed scaling allows the scaling to be fixed.

Spectrum Scale — Displays a scale below the spectrum.

Fit Parameter Show (Voxel/ROI) — If on, displays the curve-fitting results in the Info Messages window when a voxel select is performed on MVS Curve Fit data.

Misc Menu

The Misc menu on the CSI Command panel contains the following options.

Error Messages Option

When selected, the Error Messages option opens an Error Messages text window, which is scrollable so that all previous error messages can be viewed.

If there is an error, the window is automatically opened on the screen. The window can remain open or it can be closed. Error messages can be saved into a file or all messages can be deleted.

Info-Messages Option

When selected, the Info-Messages option opens an Info Messages text window, which is scrollable so that all previous messages can be viewed.

This window is for outputting of information from a particular task, such as statistics. The window automatically opens when statistics or other information is output to it. The desired information can be selected and output to a file. The messages can be deleted, and the window can either be closed or moved to a different location.

VNMR Files

CSI reads VNMR raw data files for CSI processing and image reconstruction. It does not read VNMR phasefiles.

The VNMR files that can be read are not files but directories. These directories must contain a FID file and a `procpar` file. These directories can be an experiment directory or any `fid` file saved by using the VNMR `svf` command. Unlike ImageBrowser, to read a VNMR `fid` file, the FileBrowser must have selected the `fid` raw data file within the directory containing the `fid` file and the parameter file. Select the Load option in the FileBrowser to read in the raw data file and the parameter file.

CSI does not currently process arrayed data sets, except CSI data sets that use the standard `ni` arraying scheme.

VNMR Parameters

The CSI program uses certain VNMR parameters in order to process the data. The information it obtains defines the data set's size, location, orientation, field of view, and other descriptive information. If some parameters do not exist, default parameters are used in order to process the data sets.

Standard Parameters

The following standard parameters can be used by the CSI program.

`np`, `ni`, `nf`	These parameters determine the data sizes of the data set. The `flashc` program is expected to be run on any image data set. These parameters help determine the Rank and Matrix fields. No default values, but if the parameter is not found, the values in the data headers are used.
`sfrq`, `dfrq`	Transmitter and decoupler frequencies used in the `nucfreq` field. Default value is 170 MHz.

`tn`, `dn`	Transmitter and decoupler nuclei used in `nucleus` field. Default value is H1.
`sw`, `sw1`, `sw2`	Define the spectral widths. Default value is 2000 Hz.
`lro`, `lpe`	Spatial dimensions of the reference image data in centimeters. Default value is H1.
`lpe`, `lpe2`	Length of data in the phase encode directions. `lpe` is used for the medium (y) direction when processing CSI and reference image data. `lpe2` is used for the fast (x) direction when processing CSI data. In this discussion, the fast, medium, and slow directions are considered to be the order that the fast Fourier transforms are performed and are analogous to the x, y, and z directions. Default value is 8.
`thk`	Although `thk` is not in the old standard parameter sets and is an oblique imaging parameter, it is currently the only method to define slice thickness. Default value is 1.

Spatial Parameters for Non-Oblique Sequences

The location for these data sets is currently always assumed to be at (0,0,0) coordinates.

`orient`	String parameter used with `gro`, `gpe`, `gpe2` to determine orientation. Default value is `xyz`.
`gss`, `gpe`, `gpe2`	The signs of the gradient values, along with the `orient` parameter are used to determine the orientation of the data set. These are used for CSI data sets. Default value is 1.
`gss`, `gpe`, `gro`	Gradient parameters used to determine the orientation for reference images. Default value is 1.

Spatial Parameters for Oblique Sequences

`psi`, `phi`, `theta`	Euler angles to determine data set orientation. Default value is 0.
`pss`, `ppe2`, `ppe`	Position parameters for CSI data sets. Default value is 0.
`pss`, `pro`, `ppe`	Position parameters for reference image data sets. Default value is 0.

FDF Files

The CSI tool saves data as FDF (Flexible Data Format) files. The FDF file consists of a header and data:

- The header is an ASCII header and its fields are defined by a Data Definition Language (DDL). The ASCII header makes it easy to decipher the image content and makes it easy to add new fields, and remains in keeping with the ASCII format of the *`procpar`* file.
- The data portion is binary data described by the fields in the header. It is separated from the header by a null character.

For a definition of all the fields, see the section “File Format” in the manual V*NMR User Programming*.

Creating FDF files

Use the `svsis` macro to create FDF files from VNMR and FID files saved from standard SISCO imaging sequences. `svsis` can be modified for special user-defined sequences. If standard SISCO parameters have been used, the modification can be as simple as adding a line to define the sequence. The *`svsis`* macro is described in the manual *VNMR Command and Parameter Reference*.

Another way to create FDF files is to edit or create a header defining a set of data with no headers and attach the two by using the `fdfgluer` command with the syntax:
`fdfgluer header_file <data_file <output_file>>`

This executable takes a `header_file` and a `data_file` and puts them together to form an FDF file. `fdfgluer` also calculates a checksum and inserts it into the header. If the `data_file` argument is not present, `fdfgluer` assumes the data is from the standard input. If the `output_file` name is not present, `fdfgluer` puts the FDF file to the standard output.

Splitting FDF files

The `fdfsplit` command takes an FDF file and splits the file into its data and header parts. Use the syntax :`fdfsplit fdf_file data_file header_file`. Note that the header can still have a checksum value in it. If the header does have a checksum value, remove it.

Prior Knowledge Peak Files

Prior knowledge peak picking uses files in the `$csidir/PEAK` directory to define the expected peaks and their location. Some files are already supplied for H1 and P31.

Table 9 shows a list of menu selections followed by their corresponding file names. Figure 81 shows a sample `PEAK` file for P31_standard.

Table 9. Prior Knowledge Menu Selections with Corresponding File Names

Menu Selection	*File Name*
1H in vivo standard	H1_standard
31P in vivo standard	P31_standard
13C in vivo standard	C13_standard
1H brain	H1_brain
31P brain	P31_brain
13C brain	C13_brain
1H muscle	H1_muscle
31P muscle	P31_muscle
13C muscle	C13_muscle
1H liver	H1_liver
31P liver	P31_liver
13C liver	C13_liver
31P heart	P31_heart
1H kidney	H1_kidney
1H phantom	H1_phantom
31P phantom	P31_phantom
13C phantom	C13_phantom
User defined 1 to 5	User to User5

```
#=============================================================
# P31_standard
#    Prior Knowledge of the peak information
#    Nuclei   31P
#    Tissue type: standard (in vivo)
#=============================================================
#Registered peak number
PEAK_NUM  7
#Peak ID p.p.m amplitude multiplicity J complex major shift fwhm
#PME
PEAK1    6.85    30.0      0         0.0   3     1     0.0  60.0
COMMENT1   PME
#Pi
PEAK2    4.77    10.0      1         0.0   1     1     0.6  30.0
COMMENT2   Pi
#PDE
PEAK3    2.10   100.0      0         0.0   3     1     0.0  70.0
COMMENT3   PDE
#PCr
PEAK4    0.00    40.0      1         0.0   0     1     0.0  40.0
COMMENT4   PCr
#gamma ATP
PEAK5   -2.30    30.0      2        20.0   1     1     0.3  50.0
COMMENT5   r-ATP
#alpha ATP
PEAK6   -7.46    30.0      2        20.0   1     1     0.2  50.0
COMMENT6   a-ATP
#beta ATP
PEAK7  -15.7     30.0       3       20.0   0     1     0.3  50.0
COMMENT7b-ATP
#----------------------------------------------
#!Remark:
# The order is very important. Please make sure to register peaks
#    from “lower field” to “higher field”.
#    (from higher frequency to lower frequency)
#
#Items
# “p.p.m.” is a chemical shift value [p.p.m.].
# “amplitude” is a reference. not necessary a exact value.
# “multiplicity” 1 for singlet, 2 for doublet, 3 for triplet....
# “J” is the coupling constant. [Hz] unit
# “complex” indicates a multiple peak or simple peak.
# “major” indicates a main peak or not.
# “shift” indicates how much the peak could move
#    under some physiological condition [p.p.m.]
# “fwhm” indicates Full Width Half Maximum value of the peak [Hz]
#
#COMMENTn: maximum 32 character
#-------------------------------------------------
```

Figure 81. Sample Prior Knowledge PEAK File

Chapter 7. High-Performance Auxiliary and Microimaging Gradients

Sections in this chapter:

This chapter describes high-performance auxiliary and microimaging gradients. The concept behind the high-performance auxiliary gradient (HPAG) accessory is to provide dedicated gradient coils to increase system performance. The accessory provides performance improvements for:

- Maximum gradient strength
- Gradient rise and fall times
- Duty cycle
- Eddy current compensation

These attributes provide access to higher image resolution, shorter echo times, thinner slices, faster sequences, and better localized spectroscopy lineshape in smaller voxels.

HPAG hardware is designed to provide easy and simple changeover between the system's main gradient coil and the auxiliary gradient coil. Changeover time is typically less than 20 minutes. The VNMR system software provides full support so that simple configurational changes allow the HPAG to function with all standard sequences. Pulse sequences provided by the user are easily modified for use with the HPAG gradients.

7.1 HPAG-183 Hardware

This section describes the hardware components of the HPAG-183 accessory.

Parts List

Table 10 is a list of parts that make up the HPAG-183 accessory. These parts should be received preinstalled with a new imaging system or as a retrofit kit for installation on-site by an Varian Field Service representative.

Part Functions

During installation, the gradient coil, spacing rings, and rf shield doors are adjusted and assembled to form a single unit collectively known as the *auxiliary gradient coil*. This unit

Table 10. HPAG-183 Accessory Parts List

Part Number	*Part Count*	*Description*
*	1	183-mm auxiliary coil
*	2	Spacing rings
00-967610-00	2	RF shield doors
00-967702-01	1	Gradient power cable (aux. coil)
00-967702-02	1	Gradient power cable (main coil)
00-967636-00	1	Quick-disconnect box
00-967219-91	3	Eddy current compensation boards
*	1	Probe and bore equipment kit

** Part number is different for each system and is available upon request*

is loaded into the system magnet during use and held in place on the rear flange of the system rf shield by the locking screws.

The coil is connected to the gradient supply via a gradient power cable (00-967702-01), which is cabled to the HPAG quick-disconnect box. The shim power, water, and thermocouple sensor lines are also connected to the auxiliary coil during use.

The eddy current compensation boards are calibrated during installation to provide eddy current control for the HPAG gradient coil. These boards are installed into the system gradient supply by the user when the HPAG gradient coil is in use.

A gradient power cable (00-967702-02) is cabled into the standard system gradient coil and rf shield during installation to provide quick-disconnect capability for this coil. The probe and bore equipment kit is designed to augment the standard system bore equipment to provide experimental capability for the HPAG gradient coil.

Auxiliary Gradient Coil

The function of the 183-mm auxiliary gradient coil is to provide the static and switched magnetic field gradients required for imaging and spectroscopy experiments. Figure 82 is a diagram of the coil. The gradient coil is fitted with an internal rf shield, spacing rings, gradient power cable, shim connector port, thermocouple connector, water connectors and hoses, and a locking mechanism. The following sections describe each part.

Internal RF Shield

The rf shield prevents interference from external rf sources and leakage of rf power from the system during transmission. The rf shield is completed by a pair of doors that fit on to both ends of the gradient coil.

Spacing Rings

The spacing rings are used to adjust the position of the gradient coil inside the magnet bore. These rings are adjusted during installation of the HPAG accessory to provide proper positioning of the gradient coil. If the spacing rings become misaligned for any reason, contact Varian Service to have them realigned.

Figure 83 shows a number of important connectors located on the rear housing of the coil. The functions of these connectors are described in the following subsections.

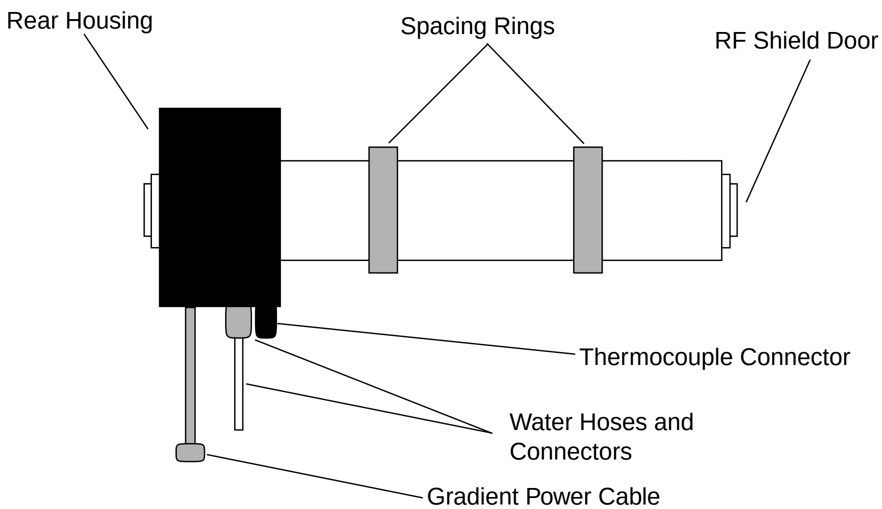


Figure 82. RF Shield Fitted on 183-mm HPAG Gradient Coil

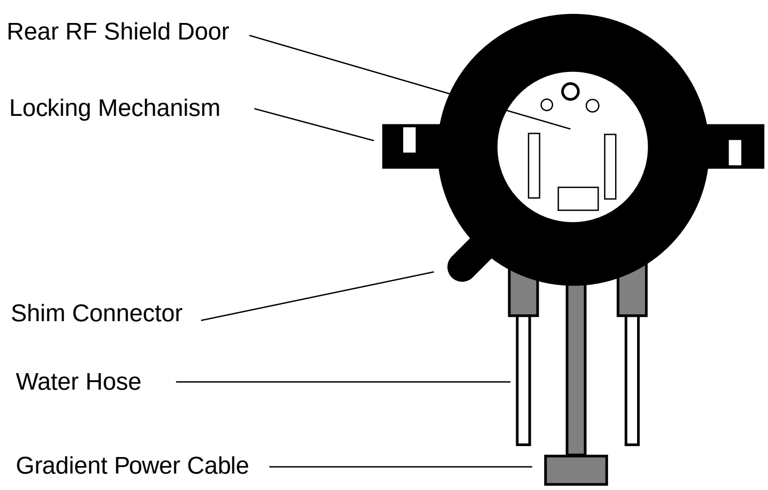


Figure 83. Rear Housing of 183-mm HPAG Gradient Coil

Gradient Power Cable

The gradient power cable (P5911) supplies power from the system gradient supply to the X, Y and Z gradient coils and shims when the cable is connected to the gradient connector port (J59X1) of the HPAG quick-disconnect box.

WARNING: **Do not connect or disconnect the gradient power cable to or from the HPAG quick-disconnect box unless both the system gradient and shim supply have been switched off. The gradient port connector of the HPAG quick-disconnect box presents a risk of electrocution if the gradient power cable is disconnected while the system gradient supply is switched on.**

CAUTION: Do not connect or disconnect the gradient power cable to or from the HPAG quick-disconnect box unless both the system gradient and shim supply have been switched off. Severe damage can occur to both gradient and shim supply if the supplies are powered up as connections are being modified.

Shim Connector Port

The shim connector port (J5912) receives power from the system shim power supply via the shim power cable (P59X2). Power is supplied to all shims except to X, Y, and Z, which obtain power through the gradient connector cable.

CAUTION: Do not disconnect the shim power cable from the shim connector port of the gradient coil unless the system shim supply has been switched off. Severe damage to the shim supply can occur if it is powered up as connections are being modified.

Thermocouple Connector

The thermocouple connector (J5913) mates with the thermocouple sensor cable (P59X3) from the system gradient supply, to complete the sensor circuits needed to protect the gradient coil from thermal overload.

CAUTION: Ensure that the thermocouple sensor cable is connected to the gradient coil you are about to use. If the sensor cable is connected to the main gradient coil when the HPAG auxiliary coil is in use or if the cable remains disconnected, the thermal overload protection circuits of the system gradient supply will not function correctly. Experiments requiring high gradient duty cycle could then lead to damage of the gradient coil.

Water Connectors and Hoses

Water hoses supply cooling water to the 183-mm gradient coil when the hoses are connected to the water fittings located on the HPAG quick-disconnect box. The quick-disconnect fittings provide automatic water shut off through spring-loaded valves located in the fittings. Shut-off allows the water supply to the gradient coil to be disconnected with minimal spillage of cooling water from the coil.

Locking Mechanism

The rear housing of the 183-mm gradient coil is fitted with locking mechanism brackets to hold the coil in the correct orientation while the coil is being used in the magnet. The holes in the brackets are located over the corresponding threaded holes located in the rear of the rf shield for the main system gradient coil. The auxiliary coil can be locked in place using the locking screws.

During installation of the HPAG accessory, the positioning of the locking mechanism brackets is adjusted to place the gradient coil in the correct orientation. If the brackets become loose or misaligned in any way, contact Varian Service to have them realigned.

HPAG Quick-Disconnect Box

The HPAG quick-disconnect box allows the power and water connections to the main system and auxiliary gradient coils to be quickly and easily interchanged. Figure 84 is a

diagram of the quick-disconnect box. The following sections describe the various connections to the quick-disconnect box.

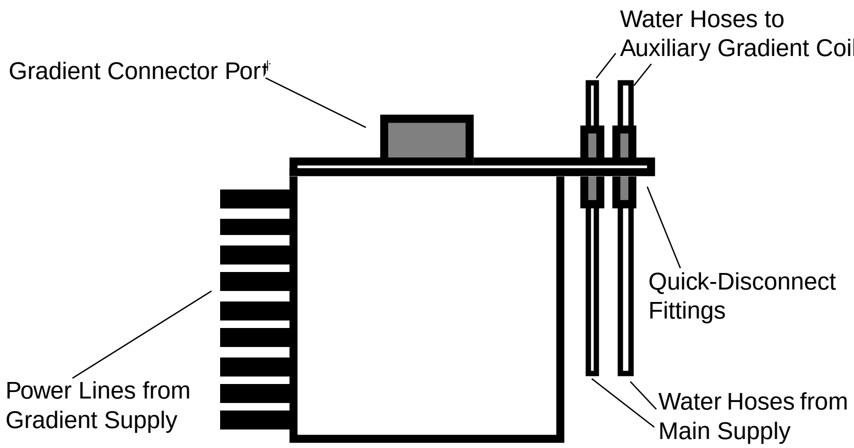


Figure 84. HPAG Quick-Disconnect Box

Gradient Connector Port

The gradient connector port (J59X1) mates with the gradient power cable from either the main system gradient coil (P5901) or the auxiliary gradient coil (P5911) to provide power for the X, Y and Z shims and gradients.

WARNING: **Do not connect or disconnect the gradient power cable to or from the HPAG quick-disconnect box unless both the system gradient and shim supply have been switched off. Gradient connector port (J59X1) of the HPAG quick-disconnect box presents a risk of electrocution if the gradient power cable is disconnected while the system gradient supply is switched on.**

CAUTION: **Do not connect or disconnect the gradient power cable to or from the HPAG quick-disconnect box unless both the system gradient and system shim supply have been switched off. Severe damage can occur to the gradient and shim supply if these are powered on as connections are modified.**

Water Quick-Disconnect Fittings

The water quick-disconnect fittings on the HPAG quick-disconnect box are connected back to the main water supply for the system. The fittings mate with the corresponding male fittings located on the ends of the water hoses supplied on the main system and auxiliary gradient coils.

Both the fittings on the disconnect box and the gradient coils have automatic spring loaded shut-off values, so that water supply can be disconnected with minimal spillage. However, it is better to shut off the main water supply when making the water connections. Shutting off the main water supply provides protection against valve failure in the fittings located in the HPAG quick-disconnect box, which would lead to a leak at full system water pressure.

Gradient Power Line Conduit

Power lines from the system gradient supply enter the HPAG quick-disconnect box through a conduit located on the inside of the box. These power lines are not part of the quick-disconnect system; regard the lines as permanent connections.

HPAG Probe and Sample Handling Equipment

The HPAG accessory includes additional probe and sample handling equipment to facilitate experiments using the auxiliary gradient coil. This equipment is designed to integrate with the main system probe and sampling handling equipment to avoid unnecessary duplication of parts. The sample handling equipment is similar to that provided for standard imaging systems equipped with 183-mm gradient coils.

System Gradient Coil

The standard system gradient coil is modified upon installation of the HPAG accessory to allow quick and simple disconnection from the system gradient and shim supplies. The water connections and hoses to the main gradient coil are also modified for quick disconnection. Figure 85 is a diagram of the modified arrangement. The functions of these connectors are described in the following subsections.

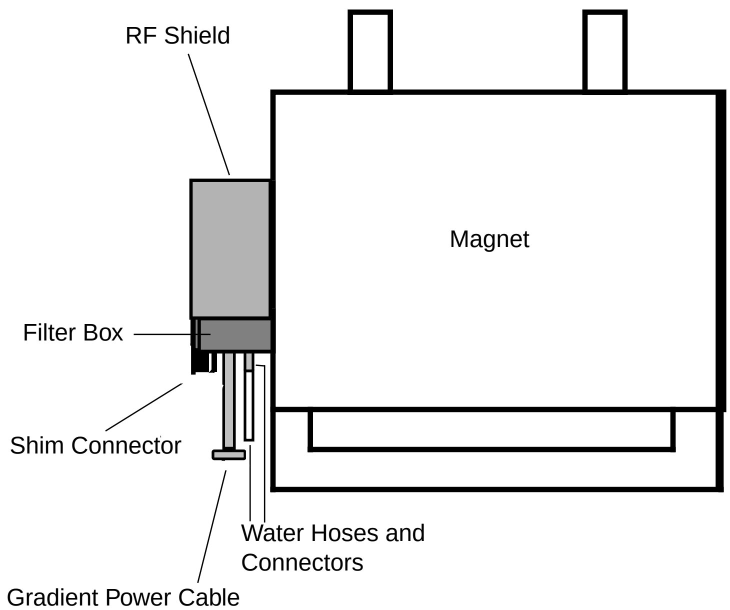


Figure 85. System Gradient Coil Detail of Connection Points

Gradient Power Cable

When connected to the gradient connector port (J59X1) of the HPAG quick-disconnect box, the gradient power cable (P5901) supplies power from the system gradient power supply to the X, Y and Z gradient coils and shims.

WARNING: Do not connect or disconnect the gradient power cable to or from the HPAG quick-disconnect box unless both the system gradient and shim supply have been switched off. Gradient connector port (J59X1) of the HPAG quick-disconnect box presents a risk of electrocution if the gradient power cable is disconnected while the system gradient supply is switched on.

CAUTION: Do not connect or disconnect this cable to or from the HPAG quick-disconnect box unless both the system gradient and system shim supply have been switched off. Severe damage can occur to both gradient and shim supply if the supplies are powered up as connections are being modified.

Shim Connector Port

The shim connector port (J5902) receives power from the system shim power supply via the shim power cable (P59X2). Power is supplied to all shims except to X, Y, and Z, which obtain power through the gradient connector cable.

CAUTION: Never disconnect the shim power cable from the shim connector port of the gradient coil unless the system shim supply has been switched off. Severe damage to the shim supply can occur if it is powered up as connections are being modified.

Thermocouple Connector

The thermocouple connector (J5903) mates with the thermocouple sensor cable (P59X3) from the system gradient supply, to complete the sensor circuits needed to protect the gradient coil from thermal overload.

CAUTION: Make sure that the thermocouple sensor cable is connected to the gradient coil you are about to use. If the sensor cable remains disconnected, the thermal overload protection circuits of the system gradient supply will not function correctly. Experiments requiring high gradient duty cycle could then lead to damage of the gradient coil.

Water Connectors and Hoses

When connected to the water fittings located on the HPAG quick-disconnect box, the water hoses supply cooling water to the main gradient coil. The quick-disconnect fittings provide automatic water shut-off, through spring-loaded valves located in the fittings. This allows the water connections to the gradient coil to be broken with minimal spillage of cooling water from the coil.

Locking Mechanism

The rear plate of the rf shield for the main gradient coil has threaded holes to accept the locking screws for the auxiliary gradient coil.

Eddy Current Compensation Boards

The system gradient power supply (GPS 2239) operates both the main and auxiliary gradient coils if the eddy current compensation boards for the X, Y and Z gradients are properly adjusted to suit the particular coil. To avoid readjustment of the eddy current compensation each time the auxiliary gradient coil is used, a second set of compensa-tion

boards is supplied as part of the HPAG accessory. These boards are adjusted to compensate for the eddy currents generated in the magnet frame by the auxiliary coil. Adjustment is made during the installation of the accessory. To convert the power supply for use with a given gradient coil, install only the appropriate set of eddy current compensation boards, respectively labeled as X, Y, and Z Signal Con boards.

Exchanging eddy current compensation boards involves opening the control panel of the gradient power supply and removing the existing set of boards from the internal card cage located behind the control panel.

To remove the set of boards from the internal card cage located behind the control panel, take the following steps, which correspond to the numbered callouts in Figure 86:

1. Place the system gradient supply in Standby.
2. Turn off the Main Power.
3. Remove the panel screws, and then flip down the control panel.

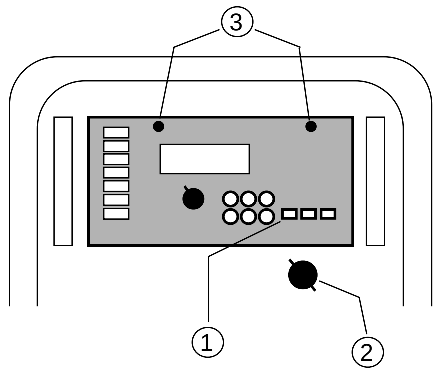


Figure 86. Front Panel of System Gradient Supply

Figure 87 shows the internal card cage, which holds the power supply control boards.

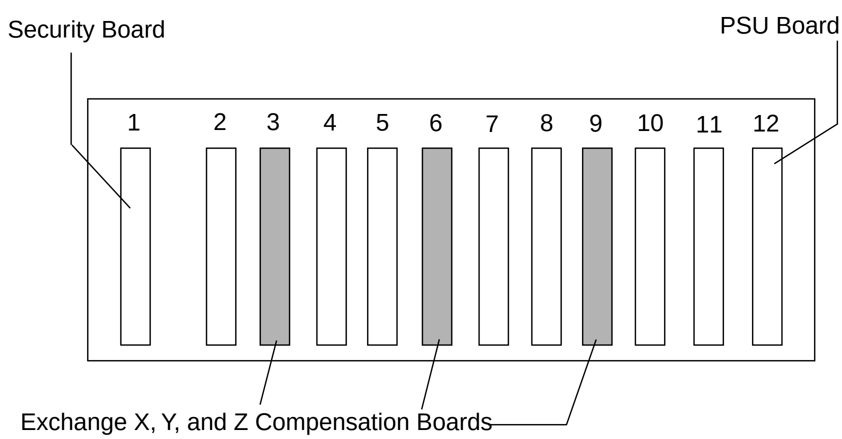


Figure 87. Gradient Supply Internal Card Cage

WARNING: **Do not proceed with the following steps unless the gradient supply is fully powered off.**

CAUTION: **The compensation boards are individually keyed to the internal card cage slots. Do not use force if the board does not fit into the slot. You could damage the boards by doing so.**

To exchange eddy current compensation boards, take the following steps.

1. Power off the system gradient supply by first pressing the “Stop” button and then turning the main power switch to the “off” position.
2. Remove the two retaining screws from the top of the gradient supply control panel and flip it down to expose the internal card cage that contains the power supply control boards.
3. Refer to Figure 87 and locate the positions of the three eddy current compensation boards. If we label the slots of the internal card cage 1 through 12 starting on the left-hand side with the security board, then the eddy current compensation boards are located in slots 3, 6, and 9. The bonds are typically labeled “X Compensation,” “Y Compensation,” and “Z Compensation.”
4. Remove the compensation board for the X gradient from slot 3 and replace it with the new X gradient compensation card.
5. Remove the compensation board for the Y gradient from slot 6 and replace it with the new Y gradient compensation card.
6. Remove the compensation board for the Z gradient from slot 9 and replace it with the new Z gradient compensation card.
7. Flip up the gradient supply control panel and replace the panel retaining screws.

CAUTION: **Power up the gradient supply only after modifying the connections to the gradient coil. If the gradient supply does not power up, check all connections again, including connections to the compensation board, shim supply, and thermocouple sensor line. If all the connections are made correctly and the gradient supply still does not power up, call Varian Service for assistance and do not proceed further.**

7.2 Experimental Setup

The purpose of this section is to describe the use of the HPAG accessory for experiments. It is important to be familiar with the individual hardware components and their interconnections.

Installing the HPAG Auxiliary Gradient Coil

This section describes how to install the HPAG gradient coil for experimental use.

WARNING: **Be aware that certain steps in the procedure are essential for safety reasons; these steps are start with the keyword SAFETY. The order of the operations is crucial; therefore, to prevent accidents and damage to the system, carefully follow the steps in order.**

1. The initial configuration of the hardware should be the same configuration shown in Figure 88, with the main gradient coil as the “active” coil. This is the standard configuration. Verify that the system is functional in the standard configuration before proceeding to install the HPAG auxiliary gradient coil.

   If the connections are not made as shown in Figure 88, the system is in an incorrect configuration and might be damaged. In this situation, perform the following three SAFETY steps and then correct the cabling error so that the connections match those shown in Figure 88. The system can then be powered up.

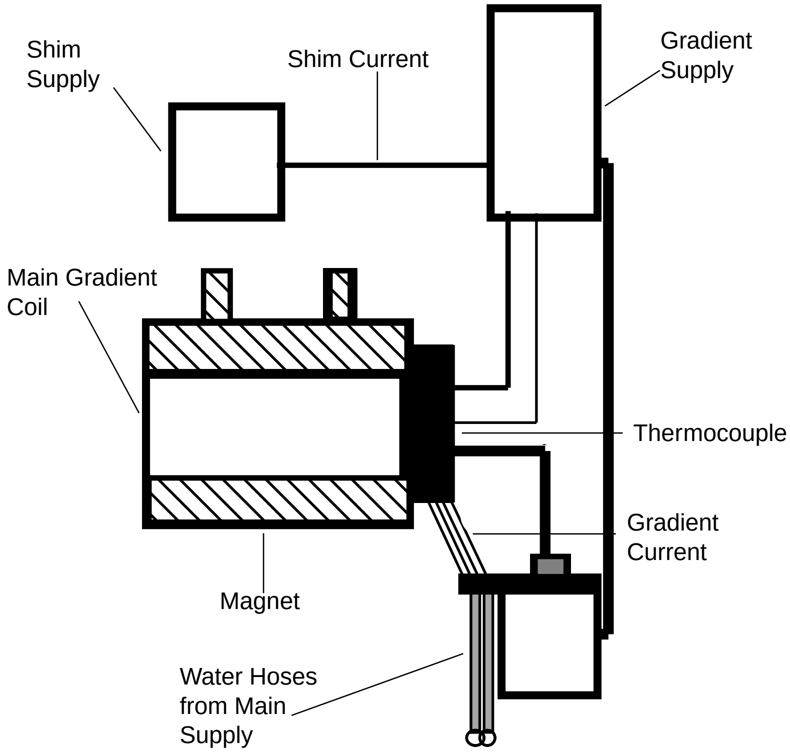


Figure 88. Connections for System Gradient Coil in Standard Configuration

2. **SAFETY:** Use the power on/off button located on the front panel of the system shim power supply to turn it off.
3. **SAFETY:** Use the STOP button and the main power switch to turn off the system gradient supply.
4. **SAFETY:** Turn off the water flow to the gradient coil at the main water shut-off valves.

WARNING: **Do not proceed with the following steps until the three previous steps, marked SAFETY, have been performed.**

5. Remove the rf shield doors from the front and back of the main gradient coil and any samples or bore equipment present in the magnet. Set aside for future use.
6. Load the auxiliary gradient coil into the magnet through the rear entrance. The auxiliary coil is heavy—use at least two people to lift and manipulate it into position.
7. Align the locking mechanism brackets on the auxiliary coil with the threaded holes in the main coil rf shield and lock in place with the locking screws.
8. Disconnect the thermocouple sensor cable (P59X3) from the main gradient coil (J5903) Connect it to the auxiliary coil (J5913).
9. Disconnect the shim power cable (P59X2) from the main gradient coil (J5902). Connect it to the auxiliary coil (J5912).

10. Disconnect the main gradient power cable (P5901) from the HPAG quick-disconnect box (J59X1). Connect the gradient power cable (P5911) from the auxiliary coil in its place.
11. Disconnect the water hoses from the main coil. Connect the water hoses from the auxiliary coil to the water quick-disconnect fittings at the HPAG quick-disconnect box.
12. Restore the water supply to the gradient coil at the main water shut-off valve. Check the HPAG quick-disconnect box for potential leaks.
13. Exchange the eddy current compensation boards in the system gradient supply for the set calibrated for the auxiliary gradient coil.
14. Verify that system connections are in the (auxiliary) configuration shown in Figure 89. before powering on the system shim and gradient power supplies.

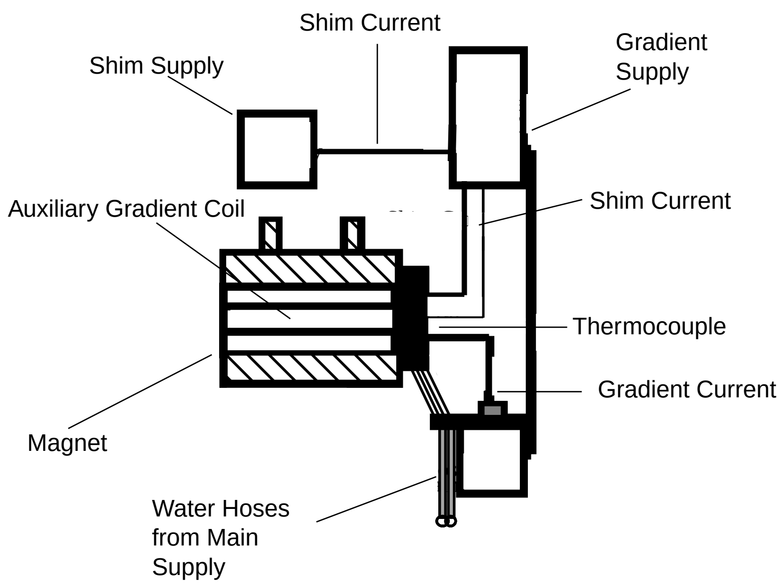


Figure 89. Connections for Auxiliary Configuration

15. The Z0 shim (manual operation only) can be reset to a value that places the transmitter offset for proton observation close to zero frequency. Otherwise, remember to compensate for the frequency shift that will be observed when using the auxiliary coil.

Removing the HPAG Auxiliary Gradient Coil

This section describes how to remove the HPAG auxiliary coil from the system and switch over to using the main system gradient coil.

WARNING: **Certain steps in this procedure are essential for safety reasons. These steps are marked with the keyword SAFETY. The order of the operations is crucial; therefore, carefully follow the order to prevent accidents and damage to the system.**

1. The system configuration is assumed to be as shown in Figure 89. This is the auxiliary configuration. Verify that the system is functional in the auxiliary configuration, before proceeding to remove the HPAG auxiliary gradient coil.

   If the connections are not made as shown in Figure 89, then the system has been left in an incorrect configuration and might possibly be damaged by the procedure. In this situation, perform the following three SAFETY steps and correct the cabling error so that the connections correspond to those shown in Figure 89. The system can then be powered up.

2. **SAFETY:** Turn off the system shim power supply using the power on/off button located on its front panel.

3. **SAFETY:** Turn off the system gradient supply using the STOP button and the main power switch.

4. **SAFETY:** Turn off the water flow to the gradient coil at the main water shut-off valves.

WARNING: **Do not proceed with the following steps until the three previous steps, marked SAFETY, have been performed.**

5. Disconnect the thermocouple sensor cable (P59X3) from the auxiliary gradient coil and connect it to the main gradient coil (J5903).

6. Disconnect the shim power cable (P59X2) from the auxiliary gradient coil (J5912) and connect it to the main gradient coil (J5902).

7. Disconnect the auxiliary coil gradient power cable (P5911) from the HPAG quick-disconnect box (J59X1) and connect the gradient power cable from the main coil (P5901) in its place.

8. Disconnect the auxiliary coil water hoses from the HPAG quick-disconnect box. Reconnect the water hoses from the main gradient coil.

9. Remove any samples and bore equipment from the auxiliary gradient coil. Set aside for future use.

10. Remove the locking screws from the locking mechanism brackets and slide the auxiliary gradient coil out of the magnet through the rear entrance. The auxiliary coil is heavy and requires the help of an additional person to lift and manipulate it. Set aside the locking screws for future use.

11. Restore the water supply to the gradient coil at the main water shut-off valve. Check the HPAG quick-disconnect box for potential leaks.

12. Exchange the eddy current boards in the system gradient power supply for the set calibrated for the main gradient coil.

13. Verify that the system connections are in the standard configuration shown in Figure 7 before powering on the system shim and gradient power supplies.

14. The Z0 shim (manual operation only) can be reset to a value that places the transmitter offset for proton operation close to zero frequency. Otherwise, remember to compensate for the frequency shift that will be observed when using the main gradient coil.

15. Replace the system rf shield doors on the front and rear of the main gradient coil after loading the bore equipment in to the magnet.

HPAG Software Support

This section outlines the software support for the HPAG accessory provided by the Spectroscopy Imaging Systems 90.1 release of system software. This software release marks a major change in the handling of gradient calibration parameters, so that a variety of new gradient coil types can be supported. Features relevant to the control of the HPAG gradient are as follows:

- Parameter `gcoil` has been created to allow the following five gradient coil dependent parameters to be rapidly set to values appropriate for the "active" gradient coil:

  `boresize griserate gxcal gycal gzcal`

  The value of `gcoil` is a string that identifies a text file in the directory `$vnmrsystem/gradtables`. The contents of the text file are the values of the five coil parameters. Altering the value of `gcoil` automatically updates the values of all five parameters to the values specified in the corresponding text file. If desired, values for any of the gradient coil dependent parameters can be entered manually, without forcing an automatic update of the other parameters.
- Gradient calibration parameters `gxcal`, `gycal`, and `gzcal` have been moved from the global file `vnmrsys/global` to the `curpar` and `procpar` files of parameter sets, FIDs and experiment directories. The parameters now have the status of "local" acquisition parameters rather than "global" configuration constants. They are transferred by the `svf` and `svp` commands, the same way as other acquisition parameters. The `rt` and `rtp` commands create these parameters if they do not exist when "older" parameter sets are recalled. The values of these parameters are in units of G/cm/DAC unit (i.e., the value of the gradient strength per unit step of the output DAC used to drive the gradients).
- Parameter `boresize` has been moved from `vnmrsys/global` to become a "local" acquisition parameter. Its value is the inner diameter of the "active" gradient coil, in centimeters.
- Parameter `B0` has been moved from `vnmrsys/global` and is now an acquisition parameter. Its value is the strength of the static magnetic field, in gauss.
- Parameter `griserate` has been created to accommodate the different rise time characteristics of the different gradient coils that can be used by a system. `griserate` holds the value of the proportionality constant between the gradient strength (expressed in DAC units) and the ramp time from/to the zero gradient (expressed in seconds):

  ramp time = `griserate` × gradient strength

  The value of `griserate` is expressed in units of sec/DAC unit. The main function of `griserate` is to measure of the system slew rate. Some pulse sequences use it for computing timing and gradient levels to refocus the NMR signal.

Running Experiments

This section describes the changes in operation of the applications environment caused by installation of the HPAG accessory. You must first be familiar with normal system operation in the standard gradient coil configuration in the absence of the HPAG accessory. The HPAG accessory changes only minor details of system operation.

1. The previously described software features allow parameters to be quickly reconfigured to accept the use of different gradient coils. After changing gradient

coil configuration, reset the `gcoil` parameter to a value corresponding to the current configuration. Table 11 lists `gcoil` values:

Table 11. Values of Parameter `gcoil`

Main Coils (Standard Design)	*System*
std18	300/183
std31	85/310, 100/310
std33	200/330
std40	200/400
Main Coils (Actively Shielded Design)	
shd18	300/183
shd31	85/310, 100/310
shd33	200/330
shd40	200/400
HPAG Accessory Coils	
hpag18	85/310, 100/310, 200/330, 200/400

2. Changing the value of `gcoil` resets the gradient coil-dependent parameters in the current experiment. Reset the following gradient levels to appropriate values for experimental conditions:

   `gpe gro gror gss gssr` **or** `gx gy gz gxr gyr gzr`

   In general, the values of the gradient parameters need to be reduced when using the HPAG gradient coil, because the coil intrinsically produces higher gradients for the same DAC setting than the main coil.

3. Other parameters affected by the change of gradient coil hardware are the following frequency parameters:

   `resto tof slcto delto` **or** `tox to toz`

   These parameters change either because of the different Z0 sensitivities (`resto`, `tof`) or because of different gradient strengths. Determine the appropriate parameter values and reset them in the normal way.

The programs `multislice`, `setgpe`, `setgro`, `setgss`, `setpoint`, etc. remain fully functional in the 90.1 software release and can be used the same way as they are used in previous software releases.

To help speed up the gradient coil changeover process:

- Reset the Z0 shim to place the resonance offset for protons (water) to a standard value, which is the same for both gradient coil configurations. Resetting the shim reduces the time needed to recalibrate the resonance frequency and helps reduce confusion over frequency offsets when using the different configurations for multinuclear experiments. Keep a record of the Z0 shim values. Place a copy of this record on or at the shim supply.
- Prepare custom parameter sets for commonly used experiments for both standard and auxiliary gradient coil configurations. Custom sets reduce the time needed to reset the parameters and decrease the probability of set-up mistakes.
- Save a basic set of shim values for some standard object such as a large uniform phantom for each gradient coil configuration. Load the set before reshimming after the

hardware change over. A saved set of shim values reduces the need to shim from "scratch" each time the gradient coil configuration is changed.

- Post a copy of the procedure for exchanging gradient coils so that it is always available to users.

7.3 Performance Specifications

The purpose of the HPAG accessory is to provide an auxiliary gradient coil that can be easily connected to and disconnected from imaging system. The auxiliary gradient coil provides access to higher gradient strengths and faster slew rates. The smaller diameter of the HPAG auxiliary coil leads to a reduction in the level of eddy currents induced in surrounding metal parts, in particular, the magnet cryostat. The effects of eddy currents are compensated by three additional compensation boards calibrated for the auxiliary gradient coil and by physical adjustment of the coil position within the magnet. Cabling to both the standard and auxiliary gradient coils is routed through the HPAG quick-disconnect box, allowing connections to be easily made to either coil.

Gradient Coil Physical Dimensions

On all systems, the inner diameter is 123 mm and the outer diameter is 183 mm.

Table 12 gives the length and weight for standard systems

Table 12. Gradient Coil Length and Weight.

System	*Length (mm)*	*Weight (kg)*
200/400 Mk II	2005	47
200/330 Mk II	1888	44
200/330 Mk III	1680	38
85/310	1368	33

Gradient Strength

The gradient strength is 10 G/cm (100 mT/m) on the X, Y, and Z axes.

Gradient Rise Time

Gradient rise times of 500 µs to 10 G/cm on X, Y, and Z axes. This time is equivalent to a gradient slew rate of 200 T/m.

Duty Cycle and Heat Dissipation

Table 13 summarizes the duty cycle specification for simultaneous use of all three gradient channels:

Table 13. Gradient Channels Duty Cycles

Gradient (G/cm)	*Duty Cycle (%)*
3	100
5	50
10	10

Eddy Current Compensation

Eddy current compensation uses exponential preemphasis signal conditioning. The compensation boards have the capacity to set five time constant and amplitude values for the preemphasis. These are calibrated for the system lifetime upon installation.

Shim Coils

The shim set for the auxiliary gradient coil has windings for Z0, Z1, Z2, Z3, Z4, X, ZX, Z2X, Y, ZY, Z2Y, XY, X2-Y2, ZXY, and Z(X2-Y2) shims.

Imaging Coil

The imaging coil has a nominal diameter of 8 cm with a 90° flip time of less than 100 µs for a square pulse. The coil is tuned at the following system proton frequencies:

- 200.057 MHz for 200/330 and 200/400 systems
- 85.500 MHz for 85/310 systems

7.4 Microimaging Hardware

The principal unit of the microimaging module is the cabinet containing the gradient control system, shown in Figure 90, which contains the gradient control circuits and power amplifiers. The power amplifiers supply the high-current pulses to the gradient coils in the magnet bore. The microimaging module installation manual describes microimaging hardware in detail.

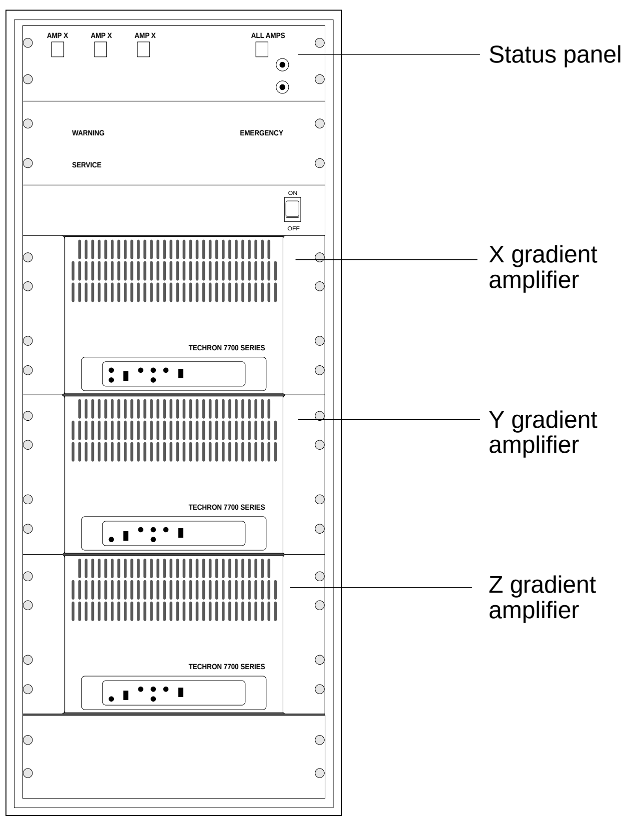


Figure 90. Microimaging Cabinet with Gradient Control System

Gradient Control System

The gradient system consists of the following hardware, which, with the exception of the gradient coils and Gradient Junction Unit, are contained in a separate cabinet:

- Gradient waveform generators that provide 16-bit amplitude control for gradient pulse shaping.
- Gradient compensation (preemphasis) units that compensate for eddy current artifacts in the gradient pulses, each with five time constants and associated amplitudes.
- Gradient power amplifiers (three required) that drive the large pulse currents through the gradient coils.
- Gradient coils assembly mounted in the magnet bore, usually inside the shim coils.
- Gradient Junction Unit.

Eddy Current Interface

Eddy currents are set by two mechanisms: the macro `eddysend` and the window interface `eccTool`. The next section, "Gradient Compensation Board," describes the controls relevant to gradient compensation, while the remaining sections describe the interface to those controls. The gradient compensation boards become programmed only when an `su` command is entered after a program or macro has been run to update the boards. Table 14 lists the macros described in this section.

Table 14. Eddy Current Interface Commands and Parameters

Commands	
`eccsend`	Create eddy current setup file
`ecctool`	Open the eccTool window
`eddysend<(file)>`	Update acquisition eddy current settings
Parameter	
`curecc` {string}	Name of eddy current compensation file

Gradient Compensation Board

Each gradient compensation board controls one channel only. Each board has five exponential pre-emphasis functions, a duty cycle limiter, a slew rate control, and an overall channel gain control (see Figure 91 and Figure 92). The pre-emphasis function adds up to five exponential waveforms to the input (demand) signal. The controls are the values of the time constants themselves and the percent response (amplitude). The circuitry then drives the gradient current to compensate for the loss in gradient field from induced eddy currents. The overall adjustment process is not detailed here. The time constants are absolute values in milliseconds and the response amplitude from 0 to 100 referenced to the amplitude of the input signal.

The gain control sets the overall channel gain, effectively establishing what current will be produced for a given demand input. This control allows the resolution in the experimenter's demand voltage to remain independent of the range of gradient currents. The gain control is linear with 100% giving the maximum current when the input voltage is full scale. This control changes the system calibration and the value of the matching shim current because the gradient coils are (often) the linear shims. If value of the matching shim current is changed, the system `gcal` value may be in error and the linear shim will need to be re-adjusted. Setting gain to just over maximum common usage, such as 10% over, helps

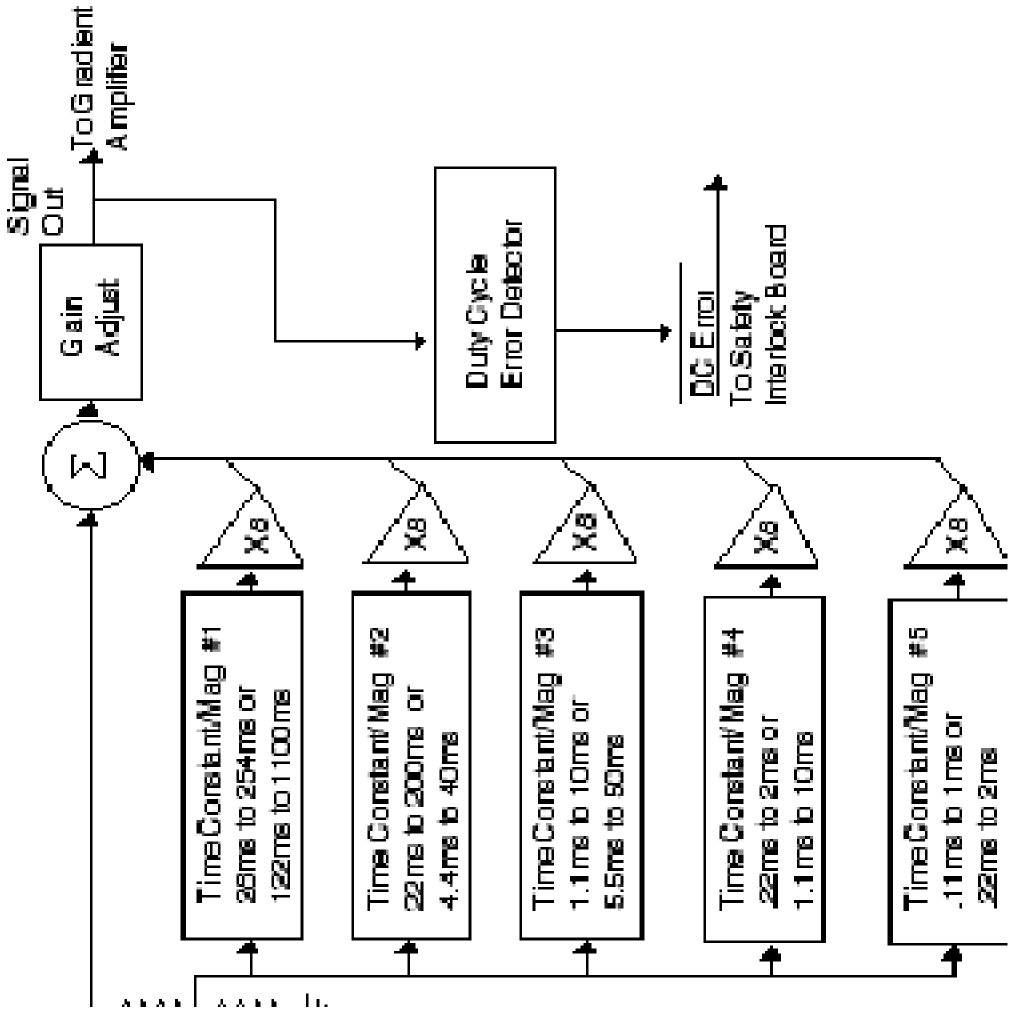


Figure 91. Gradient Compensation Signal Flow

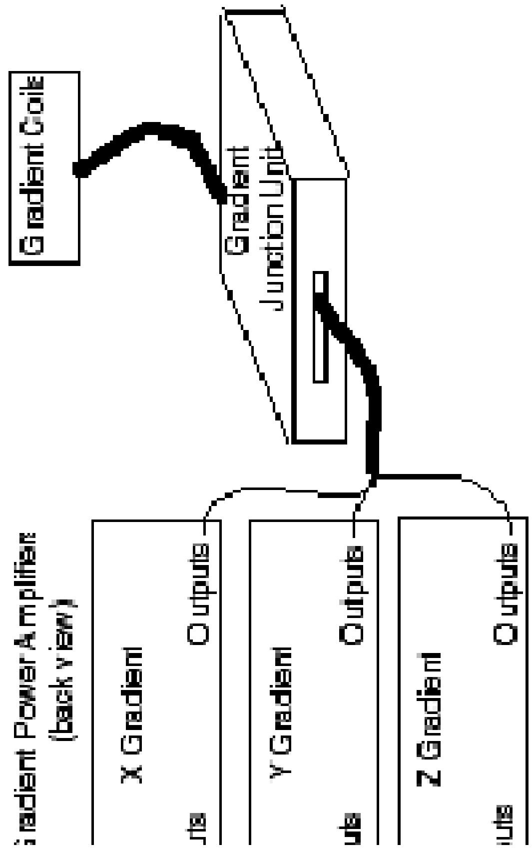


Figure 92. Gradient System Cabling

improve gradient resolution and avoids compression of the preemphasis portion of gradient pulses. Gain values of 50% are typical.

Duty cycle is a root mean square of the output voltage of the gradient compensation unit (GCU) over 100 ms. If the duty cycle is above 80%, the system is disabled; a typical safe value is a 30% duty cycle. The control is not linear in power but in the square root of power. It is linear in the output current. Values above 80% effectively turn off the duty cycle limit function. When the programmed limit is exceeded, error lights will flash on the front of the gradient compensation unit and safety interlock board will disable the gradient power supply. The LED on the gradient compensation board will be lit when the duty cycle is exceeded. The safety interlock board latches to error and will show errors with unblinking LEDs on the status panel if the problem persists, and it will show errors with blinking LEDs if the problem was transient. The values need not be defined precisely but are important safeguards that prevent equipment damage if the settings exceed the current the gradient coils can handle.

The slew rate controls the maximum speed at which the gradient input signal may change. Its effect does not depend upon the gain setting. The slew rate can be expressed as a maximum rate at which the input value may change in voltage, as a percent of full scale demand, or as the time to achieve full scale (5 V).

Table 15 gives some settings and the corresponding slew rates. Slower slew rates decrease mechanical vibration in the probe assembly. Faster slew rates give a more accurate gradient pulse shape. The desired setting is a compromise between these two requirements. A typical value is 20.

Table 15. Slew Rate Control

Input Value	*Slew Rate (mV/µs)*	*Achieved Full Scale (µs)*
0	8.8	568.0
25	84.5	59.1
50	160.3	31.2
100	311.8	16.0

eddysend Program

The macro `eddysend<(file)>` identifies the stored data values needed by the gradient compensation boards, translates them into machine form, and executes a setup operation that programs the boards. `eddysend` without arguments uses the file name specified by the user's global parameter `curecc`.

This is particularly useful when the gradient compensation boards have not been initialized on spectrometer power up or when ensuring the previous set of compensations are used. `eddysend` with a file name as an argument causes the specified set to be sent to the gradient compensation unit and changes `curecc` to the last sent value. `eddysend` is also used by the `eccTool` program when the setup function `su` is requested.

eccTool Program

The eccTool program allows interactive review and alteration of all of the gradient compensation unit values in each channel.

Opening eccTool

To open the window shown in Figure 93, type `ecctool`.

The eccTool Window

The values of a default set of parameters or those last read are displayed as a page or form.

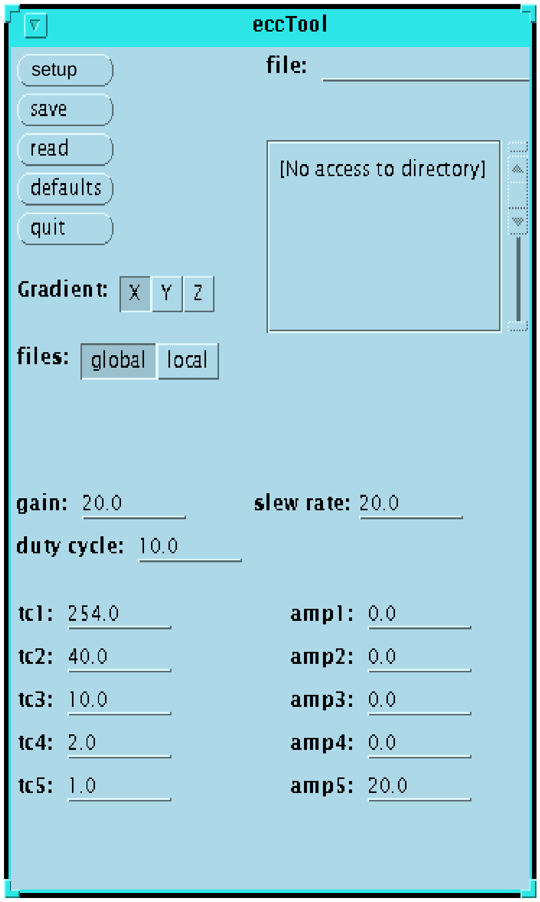


Figure 93. eccTool Window

The following information describes the control buttons that appear in the window:

setup	Takes the contents of the file named in the “file” field, translates the values into control codes, and sends the instructions to VNMR. VNMR then executes a setup. The values are finally programmed into the gradient compensation units. This button is active *only* when eccTool is started from VNMR.
save	Writes out and updates values in the file field file. When a file is written, preceding values in the file (not the window) are lost. To prevent accidental overwriting, lock a file with the files button.
read	Allows the user to read an existing file. Enter the file name or use the eccTool Files window.
defaults	Sets all values to defaults that are an uncompensated starting point.
quit	Quit the eccTool program.

Channels

The eccTool window shows the settings of one channel at a time. To display each channel in turn, click the cycle button next to the “Gradient” field.

Values

To change a value in the window, do the following steps:

1. Move the mouse to the relevant field.
2. Delete the existing field.
3. Type in the new value.

   The file name also can be manually entered. If the value is within the correct range, it is accepted. If not, an error message appears at the bottom of the window with the valid range and the erroneous value. The value should be corrected.

Accelerators

Within each field, certain keys function as accelerators:

- Typing a `?` produces a message about the valid range of the field. Additionally, typing a `d` or `D` sets the field to its default value.
- For items with a range of 0.0 to 100.0, typing `Z` sets the field to zero, typing `H` sets it to 50.0, and typing `P` sets it to 100.0.
- For time constants, typing `d` or `D` sets the value to the minimum valid value while typing `L` will set to the longest (maximum) value.

Files Window

The eccTool Files window (see Figure 94) allows you to view a list of files in a directory and to perform some limited operation upon them.

You can scroll the window to see all of the files in the `eddylib` directory.

Point to a file in the list and click the left mouse button to loads its contents in all three pages of forms.

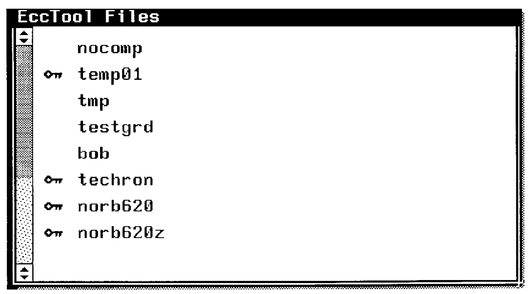


Figure 94. eccTool Files Window

The file name is highlighted and becomes the contents of the current “file” field. Preceding values in the forms are erased if unsaved.

Locking and Unlocking Files

Small key symbols to the left of the file names in the window indicate that a file has been write-protected or locked.

To lock or unlock a file (if you have permission to do so), click the center mouse button on the file to toggle the write protection.

If a locking or unlocking operation fails for some reason, the key always represents the current state of the file. The locking mechanism is designed to prevent inadvertent changes to files that might represent settings for various probes or applications.

To see a quick help reminder about write protection on files, press the right mouse button. All files in the directory appear even if they are not compensation data.

Finally, the contents of the eccTool Files window are updated only when the window is opened, so that a new file name will not show up until the window is closed and reopened.

Advanced Use of eccTool and eccsend Programs

The information in this section is most useful to those operators who want to use different gradient hardware systems that have different range requirements for the specifiers used in the eddy current compensation units.

The actual eddy current setup is performed any time the file `eddy.out` is present in the VNMR system `acqqueue` directory and `su` is typed. The content of `eddy.out` is binary data. If it is present in `acqqueue` when `su` is executed, `psg` renames `eddy.out` to `exp*.xpan.` `Acqproc` takes this file, sends it to acquisition, and then deletes it.

The file `eddy.out` is created by a program `eccsend`. This program takes a compensation file that specifies the details of the eddy current controls as text. The compensation file may be made or altered by hand or by eccTool, although manual operation of `eccsend` can send information from any location.

The gradient compensation boards default to gain and duty cycle setting of zero when powered up. The slew rate is set to zero, the compensation amplitudes are zero, and the time constants are maximum under these conditions. Therefore, any reset or power-up of the acquisition system will leave the gradient compensation boards in a safe condition. To return to the previously set conditions, the `eddysend` macro will transmit the compensation values last used by the operator and clear any error lights on the gradient system.

The ranges for the time constants may be changed in `eccsend` by hand editing the maximum time of that time constant. This mechanism is created to enable hardware changes of the time constants to be reflected into the software structure. The gradient compensation boards each have five jumpers to change the range of the time constants. A table of the jumpers and the matching time constant is furnished in the specific hardware documentation.

To match any changes to the hardware time constants, eccTool produces a header section that tells `eccsend` the ranges for its calculations. There are fifteen separate specifiers of the format `tc_{x,y,z}_{1,2,3,4,5}`, where one of the items within each of the curly brackets is chosen. The value is a floating point number in milliseconds. An example entry is as follows:

```
max time constant for X channel #1
tc_*_1     250.0
```

Mixing software and hardware time constant definitions can cause confusion. The windows time constants have default values. If the time constants are changed in hardware, the compensation file produced by eccTool must be changed manually to reflect these new values before calling `eccsend`. Old values may be present to other compensation sets, and the files should be named in a manner that distinguishes them from defaults and other probes.

The macro `eccsend` takes a text file in the subdirectory `imaging/eddylib` of the VNMR system directory and produces an output binary file. The output of eccTool is a text file that can be used as an input file for `eccsend`. Arguments for `eccsend` enable several options. The first argument is the input file name (either full or relative). If no second file name is given, `eccsend` makes a file `eddy.out` in the subdirectory `acqqueue` of the VNMR system directory; otherwise, it places that output in the named second file.

The contents of this file may be incomplete—values not set will be left alone. Lines beginning with the delimiters `:`, `#`, or `"` are treated as comments. Blank lines and lines that do not contain data are ignored. Each channel's data starts with a letter followed by a colon (e.g., `X:` or `Y:` or `Z:`).

Chapter 8. Digital Eddy Current Compensation

Sections in this chapter:

This chapter describes the digital eddy current compensation (DECC) module and decctool, the associated software interface. DECC is used in microimaging, horizontal imaging, and whole-body imaging. For setup, see the DECC installation manual.

8.1 The DECC Module

The DECC module consists of the DECC board, the Smart DAC (SDAC) board, and associated cables (a power supply is sometimes also supplied with the module in certain standalone situations.) A functional block diagram is shown in Figure 95.

DECC relies on digital signal processing technology to create appropriate compensating signals, the calculation being based on parameterized compensation requirements applied to the digital signal from the gradient wavefrm boards (WFGs). The parameters are sent to the board over the APbus. The compensating signal is scaled as appropriate and added into the main gradient signal on the SDAC, and sent out to the gradient power supplies.

The SDAC board is an improvement over previous versions of gradient DAC boards; the following signal strength and/or conditioning controls can now be set via the APbus:

- Shim input scaling
- DECC input scaling
- Rise time (slew rate)
- Output gain
- Output polarity

Also on the SDAC board is a low-power current driver that can be directly used for compensating B0 shifts. When B0 shifts are too large for this on-board current driver, a jumper setting turns the signal into voltage mode so that an appropriate external current amplifier can be used.

8.2 Theory of Preemphasis

This section is a brief theoretical description of preemphasis (also known as eddy current compensation) and is provided to orient you to the function of the module and the software, and give you a description of a few key terms. It is not intended to be a full description of

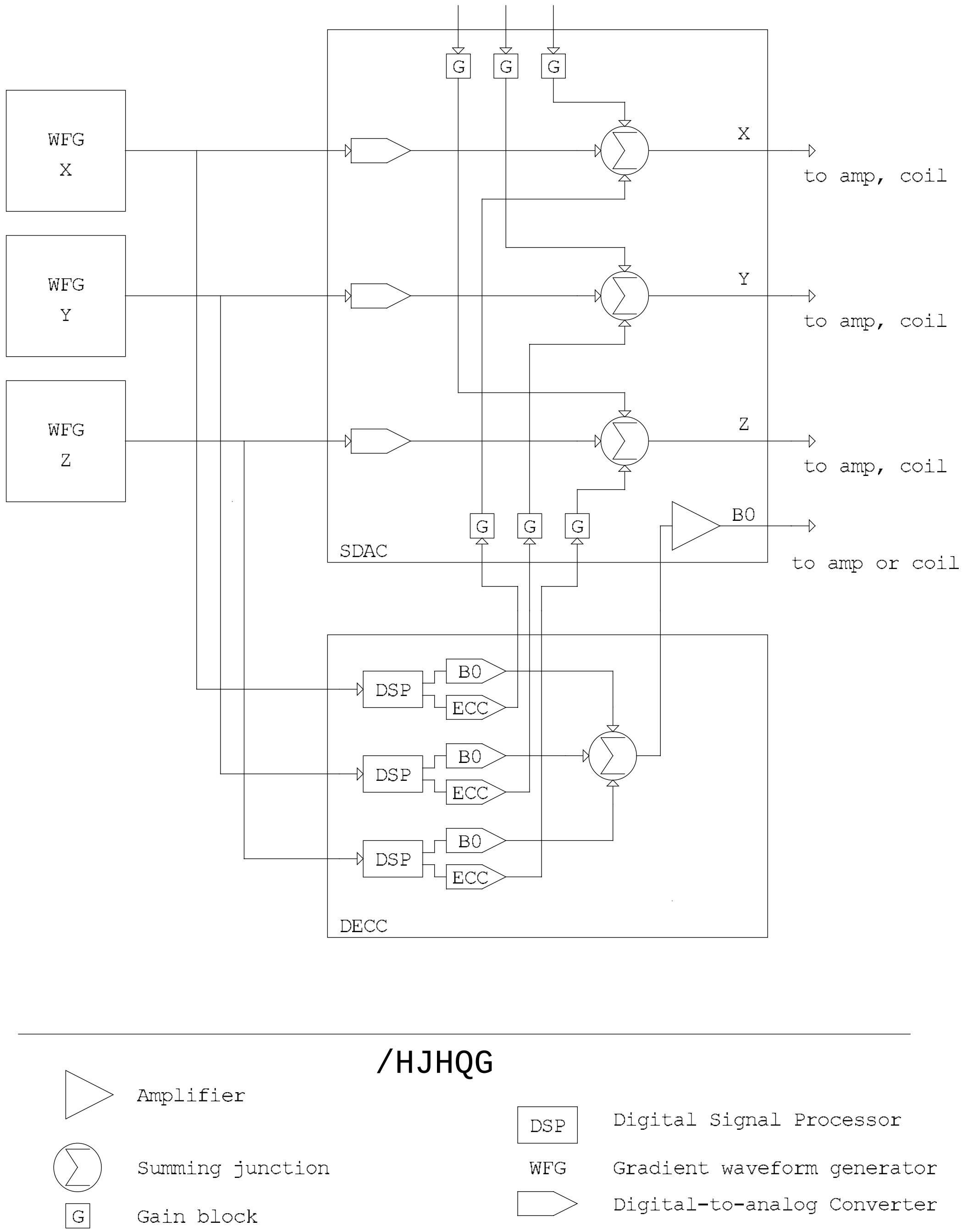


Figure 95. DECC Module Block Diagram

the issue, and you are referred to other NMR and MRI literature for more background. Also, this chapter does not provide any descriptions of methods for measuring eddy current effects.

Measuring Two Samples

Consider a configuration that consists of two samples, one (sample I) located at the center of the gradients (center of X, Y, and Z) and the other (sample II) centered in X and Y but offset from the Z center. For this simple case, assume that the samples are point-like and have very narrow linewidths. Also assume that the NMR frequency for each sample can be measured at any time and independently of each other.

A simple pulse-acquire is applied (to either sample) at a time T following a B0 field gradient pulse, as shown in Figure 96. If the rf pulse-acquire sequence is “short” compared to the gradient and eddy current times, then by varying the time T between the gradient and the rf pulse, a series of spectra result, where the spectral lines are offset from the zero-gradient spectrum and converge to the zero-gradient frequency for long time T.

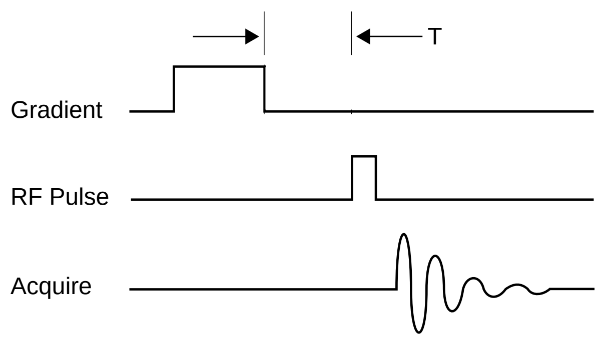


Figure 96. RF Pulse-Acquire Sequence

Experience has shown that frequency of the line as a function of time follows:

[Eq. 33]

$$f(T) = f_0\left[1 - \sum_{k=1}^{N} A_k e^{-T/\tau_k}\right]$$

where A_k and τ_k are characteristic of conducting structures in the magnet, within which the eddy currents reside. According to Lenz’s law, eddy currents act to oppose the field that caused them (for shielded gradients, A_k can be negative). In general, there are several conducting structures in the magnet, and each gives rise to a term in the summation in Equation 33.

Eddy current fields contain, for all practical purposes, two components; a B0 component and a gradient component (first order or linear term). Each component consists of a set of terms which decay according to Equation 33. The B0 terms are independent of spatial position and, therefore, influence the NMR signal at sample I and II equally. However, the linear or gradient terms influence the NMR signal differently depending on the magnitude of the gradient field at I and II. In this case, we assumed that the samples are along the *z* axis and that the Z gradient is pulsed, so these terms are more specifically known as the Z–>Z main terms. Also, for this example, the terms that cause the B0 shift are known as the Z–>B0 terms.

When the gradient is applied along one of the other axes instead of along the *z* axis, there quite often also arise gradients in the *z* axis (or “cross terms”). For sample I and sample II

oriented along *z*, the effect of an applied pulse along the *x* axis is caused by the X–>Z cross terms and the effect of an applied pulse along the *y* axis is caused by the Y–>Z cross terms.

In summary, a variety of main terms, cross terms, and B0 terms make up the eddy current effects. These effects can be corrected with DECC.

8.3 Using the decctool Interface

This section describes how to use the decctool interface. Table 16 lists commands, macros, and parameters related to the program.

Table 16. decctool Macros, and Parameters

Macro	
`deccgo`	Perform an action for decctool.
`decctool`	Open decctool window.
Parameter	
`deccgo`	Action to perform for decctool.

Opening decctool

1. To start decctool, enter `decctool` in the VNMR command window.

   The window shown in Figure 97 opens.

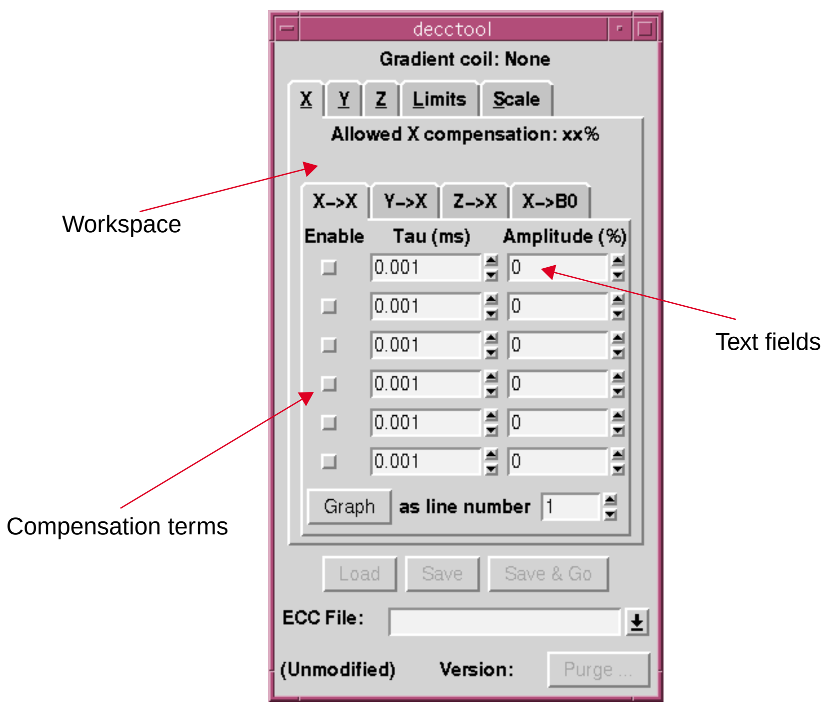


Figure 97. decctool Window

2. Click in the **ECC File** field to activate it. Type a name of your choice, then click on the **Save** button. **Do this step now before proceeding**.

Loading and Saving Files

At the top of the decctool window there is a reference to the name of the magnet gradient coil, which is the value of the `sysgcoil` parameter (“None” in Figure 97). The master file name internally used to hold the ECC values is named after the coil used, because the compensation parameters are associated with the coil-magnet combination in use.

When the decctool window opens, the values for the parameters are those in the master file, and there is no name in the **ECC File** field. In the **ECC File** field, you can enter a filename, of your choice, which becomes the scratchpad file for all of your parameter setting operations.

Notice that when the decctool window is open, the **Load** and **Save** buttons are disabled. **Load** and **Save** perform their operations on your scratchpad file and also simultaneously overwrite the master file. After you enter a file name, the buttons become active, but **do not click** on them now. Read the following sections first and familiarize yourself with the interface.

Loading a File

To load a file, type a name in the **ECC File** field, or click the pulldown menu arrow to select a file, then click on **Load**.

When you click the **Load** button, the parameters in the parameter-entry panels are simultaneously loaded from the file named in the **ECC File** field and also saved to the master file.

You can load a specific version of a file by including a version number extension in the file name (e.g., `test.7`). If you do not specify a particular version, the latest version is loaded.

Saving a File

To save a file, type a name in the **ECC File** field or click the pulldown menu arrow to select a previously named file, then click on **Save**.

When you click on the **Save** button, the parameters in the parameter-entry panels are simultaneously saved in the file named in the **ECC File** field and in the master file.

If you save over and over to a file of the same name, previous copies are kept and named with an extension incremented by one from the previous version. The number of the current version is listed below the **ECC File** pulldown menu. If you have many old files, they can be deleted by clicking on **Purge**.

When saving a file, any version number in the **ECC File** field is ignored. The version written is always one higher than the highest existing version.

Starting Experiments

The **Save & Go** button performs the same operation as the **Save** button, but also causes VNMR to start the current experiment. Until you are familiar with the operation of `decctool`, we recommend that you use only the **Save** button and start an experiment by entering `go` in the VNMR input window.

The **Save & Go** button sends the command `deccgo` to VNMR. `deccgo` is a macro that, by default, performs a `go` command. You can change the operation of `deccgo` by either writing your own `deccgo` macro or by defining a `deccgo` parameter, which will be executed by the default `deccgo` macro. For example, to make **Save & Go** execute the `au` command, enter the following commands in the VNMR input window:

```
string('deccgo')
deccgo='au'
```

Modifying X,Y, and Z Compensation Parameters

In the center of the window there is a series of panels; this area is the workspace where you can enter parameters. Across the top of the workspace are a series of tabs indicating the five main parameter entry panels. Click on the tabs to familiarize yourself with each panel. The following list briefly describes the function of each panel:

- **X** selects x-channel parameter entry (with four subpanels).
- **Y** selects y-channel parameter entry (with four subpanels).
- **Z** selects z-channel parameter entry (with four subpanels).
- **Limits** selects the panel where duty-cycle and rise time are set.
- **Scale** selects the panel where various gains are set.

Changing Time-Constants and Amplitude Values

The **X**, **Y**, and **Z** parameter entry panels are essentially the same. If you click on the tabs to select the various subpanels, you will see that there are six main compensation terms (X–>X), three in each of the two cross terms (Y–>X and Z–>X), and four B0 compensation terms (X–>B0). To change the time-constant and amplitude value for a term, do the following steps:

1. Select the text field in which you want to make the change.
2. Type in a number, or click on the up or down arrows to the right of the text field.
3. Press **Return**.

After you have pressed **Return**, notice that the message at the bottom of the decctool window has changed from “(Unmodified)” to “(Modified).” Values displayed in the various text fields that are the same as the master file are (Unmodified). Values that have changed from the master file are “(Modified).”

Selecting or Deselecting Values

Note that if you enter a nonzero value for amplitude, the **Enable** button next to the field in which you just made the change now becomes a highlighted color (if you had not previously selected the button). The purpose of the **Enable** button is to let you select or deselect values without losing track of their numeric values, as an aid in installation or troubleshooting. Upon deselection, values of zero for that particular ECC term are sent to the system.

Another installation and troubleshooting aid is a feature that lets you graph enabled values. See the section “Graphing Values,” page 205, for a description of this feature.

Setting Rise Time and Duty Cycle

The **Limits** panel is used to set Rise time and Duty cycle. These settings occur on the SDAC board. Rise time is alternatively known as slew rate. Duty cycle sets a limit for the gradient pulses—if their duration exceeds this value, an error signal is generated.

Setting Gains

The **Scale** panel is used to set various gains on the SDAC board.

The ECC gain setting affects the ECC signal coming into the summing junction on the SDAC board where the ECC is combined with the main gradient signal. Note that the value

in the X, Y, and Z parameter entry values is "what-you-see-is-what-you-get," meaning that if an amplitude of 2% is entered as an ECC parameter, then, no matter what value the ECC scale factor is in the Scale window, the 2% correction is applied to the gradient. This correction occurs because the software makes the adjustment. For the most part, you can set the ECC scale to a value and forget about it —or if the ECC scale does need to be changed, the values of the ECC parameters do not need to change. The purpose of having this scale factor available is related to resolution of the DAC creating the compensation waveform, and only in rare circumstances is the scale factor of concern.

The Shims scale factor controls the gain of the incoming shims. The x1, y1, and z1 shims are summed into the gradient signal on imaging systems.

Overall scale sets the gain on the entire set of signals—gradients, compensation, and shims. This is used mostly to correctly set the size of the image for the applied demand gradient. It accepts negative values, so it can also be used to reverse the polarity of the gradient signal.

In the Scale panel, there is a check button labeled **B0 amplitudes track Overall scaling**. When this button is on (highlighted), changing the Overall scale for an axis also changes the axis–>B0 cross term amplitudes. Changing those amplitudes is usually desirable because the B0 drive amplitude is not affected by the Overall scale and, in fact, bears no fixed relation to the amount of drive on the X, Y, and Z channels. B0 drive amplitude is unaffected because the B0 field corrections are driven by a separate coil through a separate amplifier, whereas the X, Y, and Z corrections can be set as a known percentage of the gradient strength because they modify the demand to the gradient amplifiers.

If the B0 amplitudes are set for correct B0 ECC and the **B0 amplitudes track Overall scaling** button is off, increasing the Overall scaling on an axis decreases the B0 ECC that is generated for a given linear gradient amplitude, as measured in gauss. When the button is on, the B0 amplitudes are proportionately changed to keep the correction the same. Therefore, it is important to "turn on" the tracking button if the Overall scales are "touched up" after the ECC values are set.

Graphing Values

The eccGraph window lets you graph enabled values. To open this window, do the following steps:

1. In the decctool window, select the line number (1 through 3) in the box to the right of the **Graph** button (you can display up to three functions on the graph).
2. Click on the **Graph** button. The window shown in Figure 98 opens.

The equation for each line appears in the text input fields; you can graph arbitrary functions by typing an expression into one of the boxes and pressing the **Return** key. A legend indicates the line colors used for each expression. Left-clicking the mouse on a legend entry highlights the corresponding line in the graph. In Figure 98, line number 2 is highlighted. By default, a logarithmic scale is used for the time axis, but you can select a linear scale with the scale buttons.

Zooming in the eccGraph Window

To zoom in on an area in the window, do the following procedure:

1. Click the left mouse button on one corner of the desired region.
2. Drag the mouse; notice that the cursor draws a rectangle on the graph.
3. Drag the cursor to the opposite corner of the desired expansion area and click again. To cancel the operation, second-click the right mouse button.

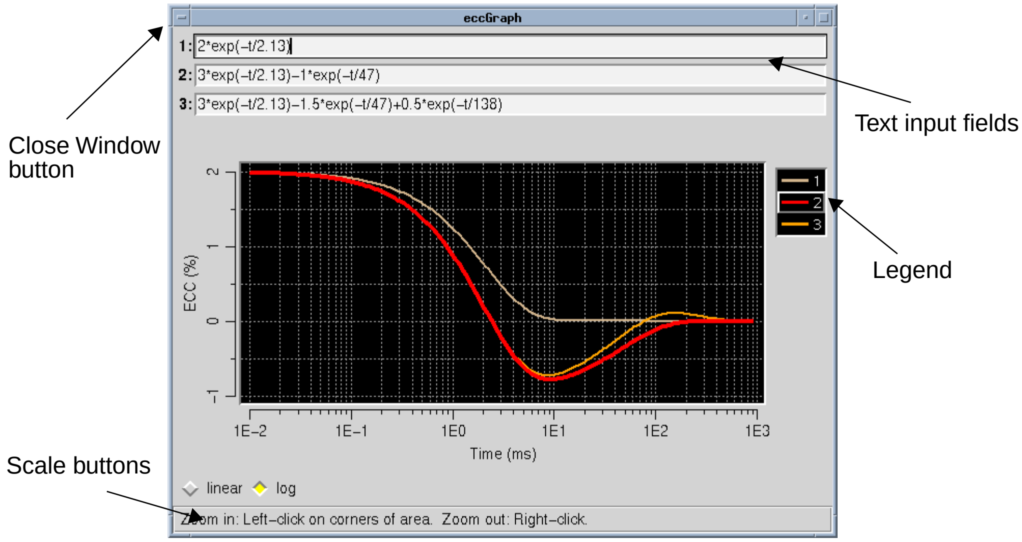


Figure 98. eccGraph Window

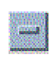
You can magnify a very small area by repeatedly zooming in on the region.

Zooming out of a Region

To zoom out of a region, click the right mouse button anywhere on the graph. You can zoom out of an region in successive zoom stages by repeatedly clicking the right mouse button.

Note that with a logarithmic time axis, zoom areas are forced to end on an even decade, so a **linear** scale must be used to zoom in on a very short time interval.

Closing decctool

To close decctool, double-click on the  button in the top left corner of the decctool frame.

8.4 Exercising decctool Using an Oscilloscope

The decctool interface and the hardware can be exercised without resorting to an actual NMR experiment. You might do this, for example, to become acquainted with the operation of the decctool window before actually performing the eddy current corrections.

Note: Perform these tests with whatever gradient power supplies are in the system turned off or to standby mode. We also recommend setting both the pulse width `pw` and the transmitter power `tpwr` to zero.

A good test sequence to use is `GDACtest.c`, although any sequence with a gradient pulse in it will work. Use the front-panel test points on the DECC board to monitor the compensation waveforms.

Chapter 9. Physiological Gating Module

Sections in this chapter:

NMR is sensitive to motion. Images from the thorax that contain moving objects, such as the heart, flowing blood, and chest wall, are often degraded by artifacts along the phase encoding, or F1, direction of the image. Referred to as *motion artifacts*, they degrade image quality, both close to the moving object (blurring) and away from the object (ghosting). With organs such as the heart, image quality is often so badly degraded that details of the structure are completely obscured. Such effects of motion upon image quality can be improved using a technique called *prospective gating*.

Prospective gating synchronizes the repetition of the imaging sequence with periodic motion of the object to be imaged. Measurement of a physical property such as the electrocardiogram (ECG) is used to provide a "physiological trigger" to synchronize the imaging sequence to the motion. Synchronization of NMR data collection with the motion period improves the image quality, because data is always collected when the moving organ is in approximately the same position. The organ appears to be static in terms of the NMR imaging process. Different aspects of organ motion can be studied by introducing a fixed delay between the receipt of the physiological trigger and the NMR data collection.

Prospective gating is similar to the use of a stroboscopic light to view a rotating wheel. If the pulse rate of the light matches the rotation period of the wheel, then the wheel appears to be static. Changing the point at which the light pulse is applied in the wheel's rotation cycle allows the wheel to be viewed in different positions.

The Physiological Gating Module 1000 (PGM-1000) detects the ECG of the experimental subject, analyzes the incoming signal, and provides a trigger pulse to the spectrometer for prospective gating experiments.

9.1 Cardiac Anatomy and Electrocardiography

This section contains descriptions of cardiac anatomy and electrocardiography. The following information might be helpful when planning and executing experiments.

Cardiac Anatomy

In mammals, the heart (see Figure 99) is a four-chambered organ located in the chest, between the forelegs of most animal subjects.

The upper chambers of the heart are called *atria* and are respectively referred to as the left and right atria. The lower chambers of the heart are called *ventricles* and are referred to as the left and right ventricles. The function of the atria is to receive blood from the *vena cava* (great vein) and pulmonary vein to contract and pump blood into the respective ventricles. The vena cava supplies deoxygenated blood from the body to the right atrium, and the pulmonary vein supplies oxygenated blood from the lungs to the left atrium.

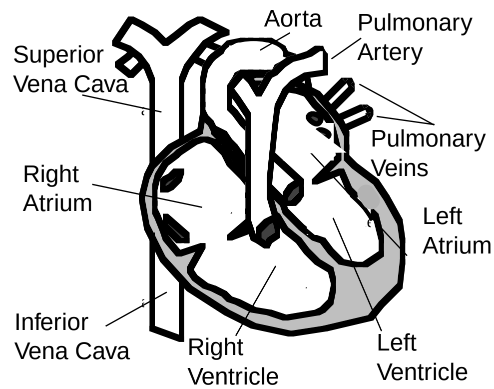


Figure 99. Cardiac Anatomy

After atrial contraction, the ventricles contract and pump blood into the pulmonary artery and the aorta (great artery). The right ventricle supplies blood to the pulmonary artery and the left ventricle supplies blood to the aorta.

The heart chambers and associated blood vessels are all visible in cardiac gated NMR images. The assignment of the ventricles from their appearance in images is quite simple. The left ventricle is usually the largest chamber of the heart and a substantial thickening of the heart wall is observed as it contracts. The right ventricle is the next largest chamber and possesses a thinner wall than the left ventricle. Both ventricles can be seen together in transverse (`orient='trans'`) and in coronal (`orient='cor'` or `'xzy'`) images.

The atria are smaller chambers than either ventricle and are easier to assign in coronal images. The atria can be seen in transverse images and, for certain slice positions, can be seen in conjunction with the ventricles. The reason for this confusing appearance is that the major (long) axis of the heart lies at an angle to the symmetry axis of the body.

Electrocardiography

The mechanical pumping action of the heart is associated with a series of electrical events that drive the contraction of the muscles in the walls of the heart. These electrical events can be detected by measuring the voltage that exists between electrodes placed at various points on the surface of the body. The appearance of the electrocardiogram depends upon the placement of the electrodes, and certain conventions have evolved to standardize the measured response.

The PGM-1000 is designed to use three standard limb leads connected to both forelegs and the right hind leg of the animal subject. With electrodes connected in these positions, the unit records an electrocardiogram corresponding to that shown in Figure 100. The result is similar to that recorded for human subjects with conventional bipolar limb leads.

The electrical waves recorded in the electrocardiogram are known as the *P*, *Q*, *R*, *S* and *T* waves, as shown in Figure 100.

The sharp spike formed by the *Q*, *R* and *S* waves is called the *QRS complex*. The *P* wave is the electrical event associated with the beginning of atrial contraction. The mechanical motion associated with atrial contraction takes place in the time interval between the *P* and *R* waves. This time is called the *PR interval* when referring to the electrical events and *atrial systole* when referring to the mechanical events. The period between the QRS complex and the *P* wave of the next cardiac cycle is known as *atrial diastole* and refers to the relaxation of the atria prior to their next contraction.

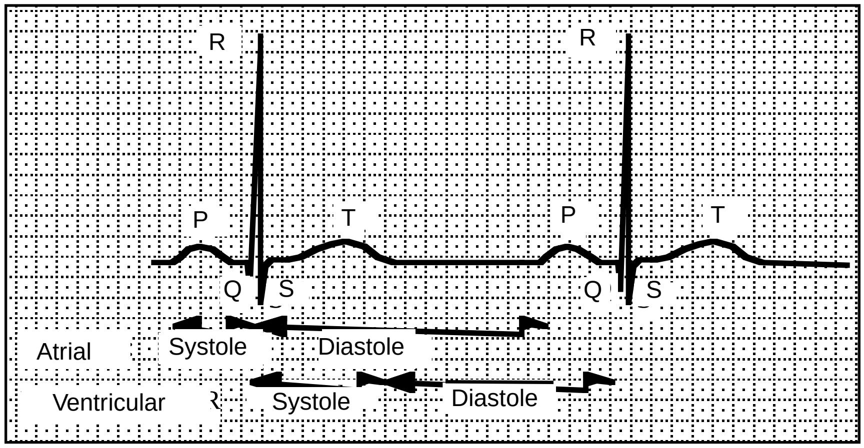


Figure 100. ECG Interpretation

The QRS complex is the electrical event associated with the beginning of ventricular contraction. The motion associated with ventricular contraction takes place in the time interval between the QRS complex and the end of the *T* wave. The interval measured for the electrical events is the *QT interval* and this time period is known as *ventricular systole* or simply *systole* when referring to the mechanical events. The ventricles are typically in the fully contracted state at the end of the QT interval. The heart is said to be *fully systolic*. The period following the *T* wave up to the next QRS complex is called *ventricular diastole* or *diastole* and refers to the mechanical events associated with the ventricles relaxing to the resting state before the advent of the next cardiac cycle. The heart becomes fully relaxed or *diastolic* just prior to the *P* wave of the next cardiac cycle.

The association between the electrical and mechanical events is known as *electromechanical coupling*. Electromechanical coupling allows prediction of the heart motion state based on knowledge of the electrocardiogram. Such a prediction is extremely helpful in setting up delay parameters, so that images can be acquired at desired points in the cardiac motion cycle. The phenomenon of electromechanical coupling leads to a link between the duration of the QT interval (ventricular systole) and the *R*-to-*R* interval or heart period. The QT interval is commonly found to be between 33% and 50% of the *R*-to-*R* interval in normal hearts.

The PGM-1000 can be adjusted to detect the QRS complex and provide a trigger pulse from the electrocardiogram. A sequence delay parameter called `hold` in the standard imaging pulse sequences can be used to delay execution of the pulse sequence after the reception of a specified number of external trigger pulses.

9.2 Hardware Description

This section describes the hardware components of the PGM-1000, including the function of all controls, jacks and ports, and PGM preamplifier battery replacement.

Parts List

Table 17 lists the parts shipped with the PGM-1000 module.

Table 17. PGM-1000 Parts List

Part Number	*Quantity*	*Description*
00-967573-00	1	PGM Receiver
00-967572-00	1	Cardiac Preamplifier (battery included)
00-967646-00	1	Cardiac Electrode Leads
67-405203-00	1	Fiber Optic Cable
00-958298-10	2	Coax Cable (short)
00-958298-20	1	Coax Cable (long)
74-122907-00	1	Preamplifier Battery (Powerdex VP/6/1400)
01-000009-00	1	Disposable Electrodes (package of 500)

Component Functions

Electrical signals generated during the cardiac cycle are detected using three disposable electrodes attached to the limbs of the animal subject. These signals are conducted to the cardiac preamplifier module (00-967572-00) via the cardiac electrode leads (00-967646-00). The cardiac preamplifier module is usually located in the magnet bore during normal operation.

Inside the preamplifier the cardiac signals are amplified and encoded for optical transmission through the optical fiber link (67-405203-00) to the PGM-1000 receiver module (00-967573-00). Inside the PGM-1000 receiver, the optical signals are reconverted and filtered. The QRS complex in the ECG is detected, using either an automatic or manual voltage threshold. Trigger pulses for gating the spectrometer are generated as each QRS complex is detected in the incoming electrocardiogram signal. A controlled number of trigger pulses can be suppressed through the use of the inhibit feature of the PGM-1000 receiver if desired. Trigger pulses are conducted to the spectrometer port J 8120, located on the system patch panel and labeled Biological Gate, through coax cable (00-958198-20).

The decoded electrocardiogram (filtered or unfiltered), inhibit output, threshold output and gate output signals can be examined using an oscilloscope connected to coax cables 00-958198-10.

Cardiac Preamplifier: Panels, Controls and Connections

The function of the cardiac preamplifier is to receive electrical signals from the three limb electrodes attached to the animal subject. The signals are amplified and encoded for optical transmission to the PGM-1000 receiver module.

Input/output jacks and the unit's controls are located on the front and back panels of the module.

Preamplifier Front Panel

The front panel of the preamp-lifier (shown in Figure 101) is fitted with the following:

- ON/OFF. This switch is used to activate the unit when it is fitted with an internal battery.

- LOW BAT. The low battery LED indicates when the power supplied by the internal battery is low. If the low battery LED blinks when the module is powered up, replace the battery before using the unit.

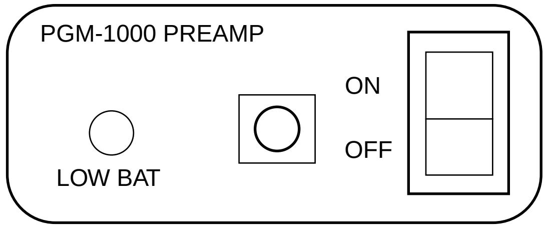


Figure 101. Front Panel of Cardiac Preamplifier

- Optical Fiber Output Jack. This jack is used to connect the unit to the PGM-1000 receiver via the optical fiber cable. It also contains a small LED used to transmit the optical signal. The LED lights on power up, unless the internal battery is exhausted.

Preamplifier Back Panel

The back panel of the preamplifier (shown in Figure 102) is fitted with three jacks that interface with corresponding colored plugs on the cardiac electrode leads.

Table 18 lists the color and connection for each jack and plug.:

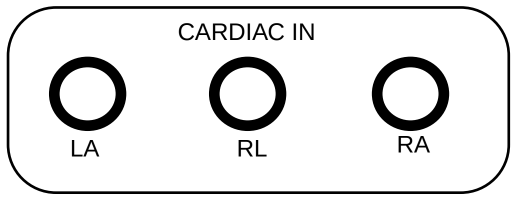


Figure 102. Rear Panel of Cardiac Preamplifier

Table 18. Cardiac Preamplifier Electrode Connections

Jack	*Color*	*Electrode Plug*	*Limb Electrode*
LA	Black	Black	left foreleg/arm
RL	Green	Green	right hind leg/leg
RA	White	White	right foreleg/arm

Internal Battery

The cardiac preamplifier is battery powered, so that it can be mounted in the animal cradle during experiments. Before any attempt to replace the battery, be sure the preamplifier is removed from the vicinity of the magnet beyond the 5 gauss line.

CAUTION: **The battery used inside the cardiac preamplifier is weakly magnetic. As a result, the unit is subject to a small magnetic force when placed close to the magnet.**

If the preamplifier is located at least 12 cm away from the image plane, the battery used to power the unit, which is weakly magnetic, should create minimal disturbance in the homogeneity of the main magnetic field.

From time to time, the internal battery in the cardiac preamplifier needs to be replaced. Symptoms that indicate battery replacement is needed include:

- LOW BAT indicator on preamplifier front panel blinks when the module is powered up. Battery power is low. Replace the battery before beginning experiments.
- LOW BAT indicator on the PGM-1000 receiver unit lights during the course of an experiment (it is assumed that the units are linked via the optical fiber and that the

cardiac preamplifier is located in the magnet). Replace the battery. The PGM system will continue to function during a low battery condition, while the PGM-1000 receiver preamplifier ON LED remains lit.

- If the preamplifier ON LED on the PGM-1000 receiver is not lit when the units are linked via the optical fiber, the preamplifier unit might not be powered up, the internal battery might be dead, or the optical fiber system has developed a fault.
- If both the LED in the optical fiber output jack and the Low Bat indicator fail to light on power up, the internal battery might be dead or the preamplifier optical fiber circuits might have failed. Check the battery and, if necessary, replace it before experiments are started.

CAUTION: **When replacing the battery, move the preamplifier away from the vicinity of the magnet bore. Keep all tools outside the 5-gauss stray field.**

To replace the battery, turn off the power to the unit and perform the following steps, which correspond with the numbered illustrations in Figure 103.

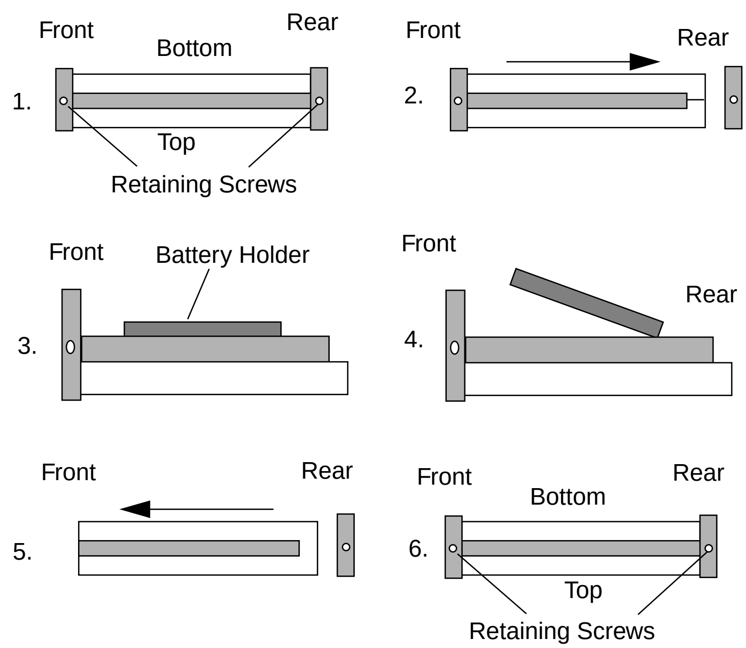


Figure 103. Battery Replacement Procedure

1. Locate and remove the two retaining screws that hold the black plastic flange around the rear panel of the preamplifier.
2. Remove the black plastic flange using a small Phillips screw driver.
3. Slide the lower cover of the unit to reveal the battery holder.
4. Lift the edge of the battery holder closest to the front panel upwards, and slide the old battery out of the holder.
5. Insert the fresh battery into the battery holder. Make sure that the metallic terminals of the battery face the side of the holder that is wired to the internal circuit board.
6. Replace the black plastic flange.

Before reassembling the unit, check the function of the new battery by turning on the power to the unit. The LED in the optical fiber jack should light and the low-battery indicator should remain dim. If this test is successful, power off the unit.

If the new battery does not cause the LED in the optical fiber jack to light during power up, then the unit has failed, the battery is incorrectly inserted into the internal holder, or the battery itself is exhausted. Try another battery. Persistent failure of the optical fiber LED to light during power up indicates a failure of the preamplifier circuits.

If the new battery provides power to the unit, reassemble the preamplifier by seating the battery holder correctly in to the base of the unit. Replace the lower cover by sliding the cover until it mates with the black flange that surrounds the front panel. Replace the black flange and retaining screws that were removed from the rear panel.

Final test the preamplifier by powering on and observing the LED in the optical fiber jack.

Receiver: Panels, Controls and Connections

CAUTION: **The PGM receiver contains several ferromagnetic subassemblies. The unit is subject to a significant force when placed close to the magnet bore and represents a hazard if brought into regions of magnetic field exceeding 30 gauss.**

The PGM-1000 receiver receives optically encoded signals from the cardiac preamplifier module and reconvert these to electrical signals. The reconverted ECG is then filtered, using a selectable bandpass filter. The QRS complex in the filtered ECG is detected, using either an automatic or manual voltage threshold. Trigger pulses are generated for gating the spectrometer as each QRS complex is detected. A controlled number of trigger pulses can be suppressed through the use of an inhibit delay feature, if desired. The decoded ECG (filtered and unfiltered), inhibit output, threshold voltage, and gate output signals can be observed with an oscilloscope. The controls for this module are located on the front panel. The input/output jacks and unit’s power cord are located on the back panel.

Receiver Front Panel

Figure 104 shows the front panel of the receiver.

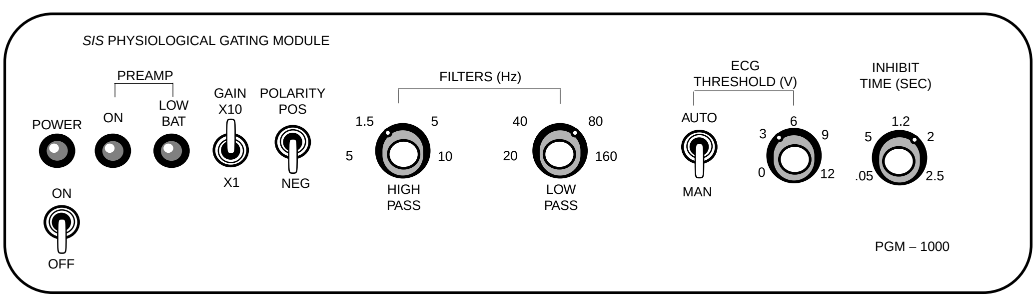


Figure 104. Front Panel of PGM-1000 Receiver

The front panel contains the following controls and indicators:

- ON/OFF activates the unit when plugged into a source of ac current at 115 V, 50/60 Hz.
- POWER ON lights to indicate that the PGM-1000 receiver is powered up.
- PREAMP:ON lights to indicate that the cardiac preamplifier is powered up and that the optical link between the modules is functional.

- PREAMP:LOW BAT lights to indicate that the power of the cardiac preamplifier battery is low. Replace the battery. The PGM-1000 units will continue to operate once the low battery condition is indicated until the PREAMP ON LED dims, indicating failure of the optical link.
- GAIN X10/X1 boosts the gain of the PGM-1000 receiver amplifier to increase the level of the decoded ECG signal. The switch has X1 and X10 positions.
- POLARITY:POS/NEG inverts the polarity of the ECG signal. The PGM-1000 receiver detection circuits only provide trigger pulses for positive signals (upward deflections on oscilloscope trace). The polarity switch can be used to adjust the ECG to the correct polarity for triggering.
- FILTERS (Hz):HIGH PASS sets the high-pass portion of the user-selectable bandpass filter. The control has multiple positions, selecting filters at 0.5, 1.5, 5 and 10 Hz. Frequencies below the selected value are attenuated in the filtered ECG signal.
- FILTERS (Hz):LOW PASS sets the low-pass portion of the user-selectable bandpass filter. The control has multiple positions, selecting filters at 20, 40, 80 and 160 Hz. Frequencies above the selected value are attenuated in the filtered ECG signal.
- ECG THRESHOLD (V) AUTO/MAN selects the type of threshold applied to detect the QRS complex in the filtered electrocardiogram. The upward setting of the switch selects the automatic threshold feature, which disables the ECG voltage level control used to select the manual threshold level. The downward setting of the threshold selection switch selects manual control of the ECG threshold level.

  The ECG Voltage Level Control is active when the manual threshold mode is selected. The threshold voltage level is continuously variable between 0 V and 12 V. Selecting the setting of the PGM-1000 receiver gain switch adjusts the amplitude of the QRS complex in the filtered ECG in this range.
- INHIBIT TIME (SEC) sets the value of the time delay used by the PGM receiver inhibit feature. The inhibit feature allows the frequency of the trigger pulses (used to gate the spectrometer) to be controlled. Increasing the inhibit delay time decreases the frequency of triggering. The inhibit delay can be set in a continuous fashion up to a maximum value of approximately 2.5 seconds.

Receiver Back Panel

Figure 105 shows the back panel of the receiver.

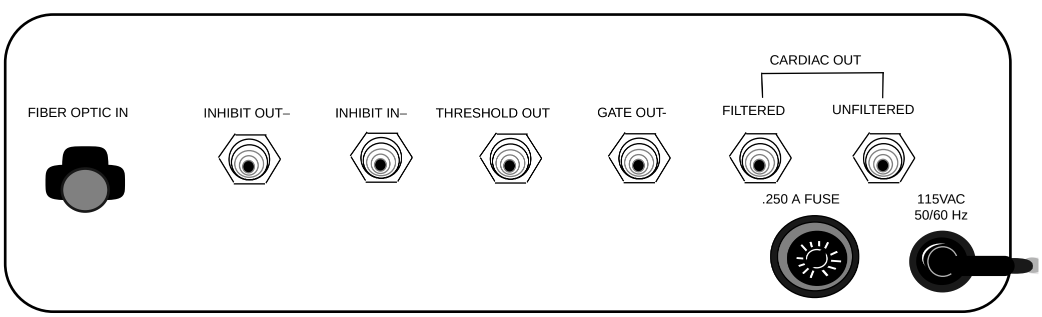


Figure 105. Back Panel of PGM-1000 Receiver

The back panel of the PGM-1000 receiver is fitted with input/output jacks as follows:

- FIBER OPTIC IN is used to connect the PGM-1000 receiver to the cardiac preamplifier via the fiber optic cable.

- INHIBIT OUT– can be used to view the inhibit delay signal used by the PGM-1000 receiver inhibit feature. The signal available on this port is held as a +5 V signal when the unit is ready to generate trigger pulses. The signal is reduced to 0 V (ground) during the inhibit delay.
- INHIBIT IN– has a voltage level that is held high, at +5 V, to permit the PGM-1000 receiver to generate trigger pulses. If an incoming signal reduces the level to 0 V (ground), the PGM-1000 receiver will be inhibited from producing trigger pulses. This feature allows an experiment (using the electrocardiogram and a signal generated by a second transducer or other external device) to be “double gated.”
- THRESHOLD OUT is the threshold voltage level used to detect the QRS complex in the electrocardiogram. The signal is a constant voltage that ranges from 0 V to 12 V.
- GATE OUT carries the signal used to gate the spectrometer. For normal operation, connect it to the port labeled Biological Gate (J8120) on the spectrometers patch panel. The gate pulse signal is held at +5 volts. This voltage is reduced to 0 V (ground) for a period of 1 ms in order to generate a trigger pulse for the spectrometer.
- CARDIAC OUT:FILTERED carries the filtered ECG signal.
- CARDIAC OUT:UNFILTERED carries the ECG signal in the unfiltered state.
- 115VAC 50/60Hz is the power cord for a 115 Vac, 50/60 Hz, power input. Suitable power output sockets are located on the rear panels of the spectrometer. Use these sockets for voltage compatibility and correct electrical grounding of the PGM-1000 units.
- .250 A FUSE holds a 0.25-A, 1.25 in. fuse. Check the fuse if the PGM-1000 receiver fails to power up.

Cardiac Electrode Leads: Electrode Connections

The set of cardiac electrode leads provided with the PGM-1000 are designed to be connected to the subject to form a standard limb lead configuration.

Connect electrodes to a region of exposed skin on the right foreleg, hind leg, and the left foreleg of the subject. Suitable signals can often be obtained from the pads on the surface of the subject’s feet. Shaved regions are suitable for obtaining ECG signals.

The self-adhesive electrodes supplied with the PGM-1000 kit require no electrode gel and can be directly applied to the bare skin. Additional tape might be required to secure the electrodes to the limbs of larger animals.

The cardiac electrode leads can be clipped to the electrode tabs in order to connect the leads to the animal. Avoid

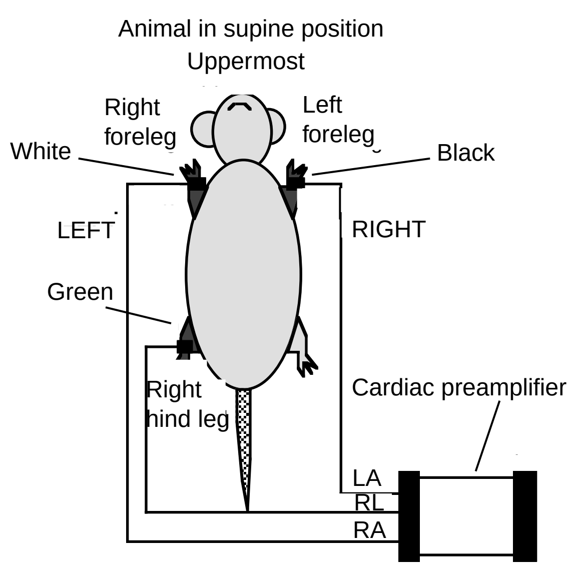


Figure 106. Electrodes Connection

clipping the electrode leads directly to the animal. A diagram showing the connections to the animal and cardiac preamplifier is shown in Figure 106.

The clips, located at one end of the cardiac electrode leads, are color coded to indicate the target limb for connection.

Clip Color	*Limb Electrode*
Black	Left foreleg or left arm
Green	Right hind leg or left leg
White	Right foreleg or right arm

Connect the plugs at the opposite end of the cardiac electrode leads to the cardiac preamplifier module. These plugs are color coded, to indicate both the corresponding limb electrode and socket on the preamp. The connections are made as follows:

Plug Color	*Socket*	*Socket Color*	*Limb Electrode*
Black	LA	Black	Left foreleg or right arm
Green	RL	Green	Right hind leg or right leg
White	RA	White	Right foreleg or right arm

9.3 Experimental Setup

The is section describes the use of the physiological gating module for cardiac gated experiments. Familiarity with the individual hardware components and the function their controls is necessary.

Hardware Preparation

This section describes assembly and connection of the PGM-1000 components to obtain ECG gated studies from the subject. A diagram showing the interconnections between the PGM-1000 modules and the system is shown in Figure 107.

1. Power up the cardiac preamplifier unit only and check the internal battery status. Replace the battery if necessary. Power down the preamplifier to avoid wasting the battery after testing.
2. Mount the cardiac preamplifier unit in one of the front slots of the animal cradle (the slots are normally used to hold rf coil tuning boxes). The edge of cardiac preamplifier should slide into the slot, so that the front panel of the unit is visible from the magnet entrance. Connect the cardiac electrode leads to the corresponding color-coded sockets on the rear panel of the cardiac preamplifier. Users who have older style probe and bore equipment can mount the cardiac preamplifier on a tuning box bracket or to the animal bed. Firmly secure the unit in place with tape. If the preamplifier is placed in the animal bed, make sure that it is at least 10 cm to 12 cm from the intended position of image slice planes.
3. Connect the optical fiber cable to the front of the cardiac preamplifier and run the cable over to the PGM-1000 receiver.
4. Mount the PGM-1000 receiver unit on top of a system cabinet. Plug the power cord of the PGM-1000 receiver into one of the spare power sockets, available on the rear of this system cabinet.

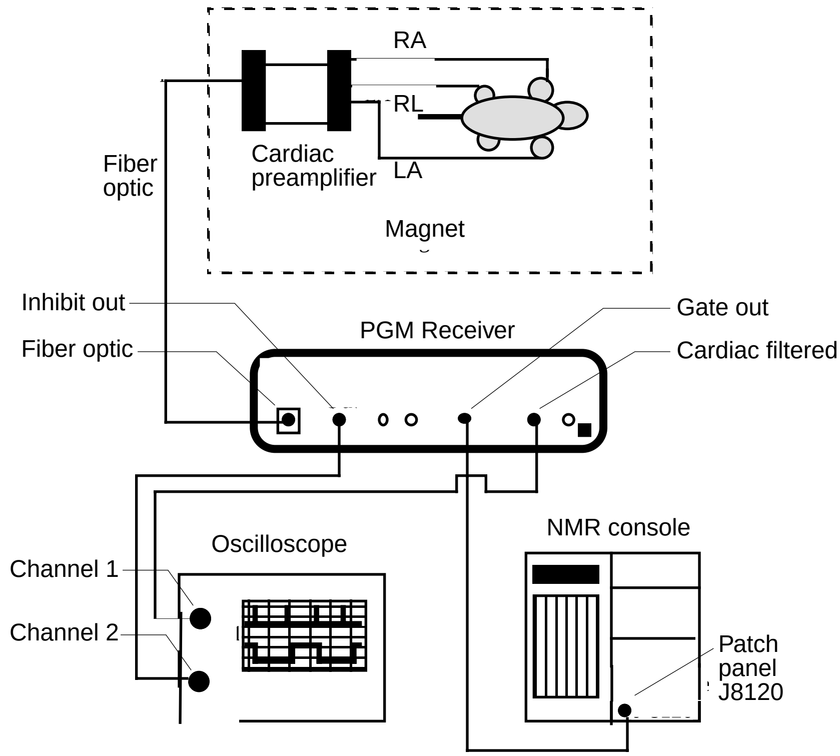


Figure 107. Unit Interconnection Diagram

5. Connect the optical fiber cable to the FIBER OPTIC input jack located on the rear of the PGM-1000 receiver. Power on both the PGM-1000 receiver and cardiac preamplifier. The PREAMP ON LED of the PGM-1000 receiver should be lit, indicating that the optical link between the cardiac preamplifier and PGM-1000 receiver has been properly established.
6. Connect the GATE OUT- jack of the PGM-1000 receiver to the input port on the spectrometer patch panel marked Biological Gate (J8120) for an external trigger.
7. Connect the CARDIAC OUT FILTERED jack to channel 1 of an oscilloscope. Adjust the channel amplitude to 0.5 V per division and select dc input.
8. Connect the INHIBIT OUT- jack to channel 2 of the oscilloscope and adjust the channel amplitude to 2 V per division. Select dc input and normal polarity.
9. Adjust the oscilloscope to dual-channel mode.
10. Adjust the oscilloscope time base control to 0.1 or 0.2 s per division. Select channel 1 as the trigger source, with normal triggering mode and ac coupling.
11. Adjust the bandpass filter controls of the PGM-1000 receiver so that the high-pass frequency is 0.5 Hz and the low-pass frequency is 160 Hz.

At this point, the hardware is prepared but the oscilloscope does not register useful signals.

Animal Preparation

Anesthetize the subject using an established method. Longer acting injectable anesthetics or controlled inhalant anesthetics are to be preferred for gated experiments because extra

preparation time is required to establish ECG gating requirements. For initial trial experiments, about 45 minutes extra time is probably required to investigate the use of the PGM-1000 receiver controls. In practical situations, persons who are familiar with the PGM-1000 require only 10 to 15 minutes extra time.

1. If the subject's feet are unsuitable for electrode attachment, make an attachment area by shaving sites on the animal's right limbs and left foreleg.

2. Place the subject into the animal bed in the supine position (ventral surface upper most). Place the center of the thorax as close as possible to the center of both the magnet and rf coil.

3. Attach the electrodes to the forelegs and the right hind leg of the animal. Connect these electrodes to the cardiac electrode leads. It is important to connect the ground (green) lead to the hind leg of the animal. Figure 106 on page 215 shows the proper electrode connection pattern. The polarity switch of the PGM-1000 receiver can be used to correct the sign of the ECG signal if the leads to the forelegs are connected in the reverse sense. Bring the electrode lead wires from the underside of the animal bed so that they can be taped to the bed surface, to prevent the wires from moving during the experiment. Securely tape the animal's limbs and electrode clips to the animal bed. These precautions minimize the disturbance observed in the ECG signal, due to small motions of the subjects limbs and vibrations of the electrode leads.

4. Before inserting the cradle into the magnet, check the electrode placement and ECG signal by powering up the cardiac preamplifier. Adjust the oscilloscope to trigger on the ECG signal on channel 1 of the oscilloscope. If the ECG is weak, increase the gain of the PGM receiver, using the X10 gain setting.

5. If an acceptable ECG signal with a QRS complex of about 1 to 1.5 V and baseline features of less than 0.5 V can be obtained, note the following features of the ECG:

   R-to-R wave time interval

   R-to-T wave time interval

   P-to-R wave time interval

   These features are useful in choosing acquisition parameters. If a poor signal is obtained, check the electrodes, electrode connections, and power on status of the PGM modules. Correct any defects in the preparation. ECG signals greater than 1.5 V can be observed. Try to scale the peak of the R wave so that it is less than 12 V.

6. Place the animal cradle into the magnet. Tune the rf coil as usual.

Adjusting the PGM Receiver to Obtain a Cardiac Trigger

Once the animal cradle has been inserted into the magnet, check the ECG signal on channel 1 of the oscilloscope. It should show slight changes after the animal cradle is placed into the magnet. Typically, the *T* wave appears with a larger amplitude and baseline noise might increase. The peak of the QRS complex should be at least 0.5 V above the largest baseline feature if an acceptable cardiac trigger is to be obtained.

Adjusting the receiver to obtain a cardiac trigger consists of the following steps:

1. Adjust the bandpass filter to obtain a stable electrocardiogram with a flat baseline.
2. Set the voltage threshold used to detect the QRS complex.
3. Adjust the inhibit delay to control the frequency of the trigger pulses.

Adjusting the Bandpass Filter

The low-pass filter control of the PGM receiver reduces the high-frequency noise in the ECG. High-frequency noise is attenuated as the low-pass frequency is decreased. Attenuation improves the signal to noise ratio of the QRS complex; although, the total amplitude of the ECG will be progressively reduced as the low-pass frequency is reduced. It is best to initially set the low-pass frequency to 160 Hz.

The high-pass filter control removes low-frequency undulations from the baseline of the ECG. Low frequencies are attenuated as the high-pass frequency is increased. The best initial setting of the high-pass frequency is 0.5 Hz.

When the recommended initial frequencies for the bandpass filter controls have been set, the electrocardiogram is close to the unfiltered state.

Increase the high-pass frequency until any baseline undulations are removed. Typical low-frequency baseline undulations have a period greater than one heart period. Baseline undulations often arise from the motion of the animals limbs due to respiration, and can be minimized by securing the limbs and electrode clips to the side of the animal bed with tape. The polarity of the QRS complex might invert for higher settings of the high-pass frequency. Correct any inversion with the polarity switch.

When the high-pass filter has been adjusted, decrease the low-pass filter only if the ECG is noisy.

Setting the ECG Detection Voltage Threshold

There are three ways to adjust the ECG detection voltage threshold. The simplest way is to take advantage of the automatic threshold feature.

- Automatic Threshold

  To set up the automatic threshold, first reduce the inhibit delay time control of the PGM-1000 receiver to the minimum value. Reducing inhibit delay time causes it to trigger on every event that exceeds the value of the ECG detection threshold. Switch the ECG detection threshold to automatic mode, while observing the inhibit output signal on channel 2 of the oscilloscope. After a few heart beats, the automatic threshold is established and the inhibit out signal begins to respond in a periodic fashion as each QRS complex is detected.

  The pattern visible in the inhibit out signal consists of a level change of 5 V (decrease from +5 V to 0 V) as the QRS complex is detected. This state is maintained for 50 ms, then the signal returns to its original level (+5 volts), until another QRS complex is detected. Such fluctuation indicates that a cardiac trigger has been obtained.

  The automatic threshold can be used to obtain cardiac gated images. However, it takes a few heart beats to recover from the disturbances induced in the ECG by rf and gradient pulses. This recovery time makes it less suitable for applications that require a short TR or high-duty cycle multislice imaging.

  The manual threshold requires no such recovery time and supplies cardiac triggering as soon as the rf and gradient disturbance has left the ECG.

- Manual Threshold

  To set up the manual threshold, first reduce the inhibit delay and ECG threshold voltage controls to their minimum value. Observe the inhibit output on channel 2 of the oscilloscope. The inhibit output signal appears to behave in an erratic fashion when the threshold voltage is close to zero. Slowly raise the value of the ECG threshold voltage, while observing the inhibit out signal. Allow a few heart beats to pass between each adjustment of the control and carefully note the point at which the inhibit output begins to respond in a periodic fashion as each QRS complex is detected.

The response of the inhibit output should be identical to the previously described response for the automatic threshold, when cardiac triggering is obtained. This is the minimum setting for the ECG detection threshold. Note the position of the threshold voltage control.

Continue to increase the threshold voltage until the inhibit output just ceases to respond to the presence of QRS waves in the ECG. The threshold is now set to the maximum point of the R wave signal. Note the position of the threshold voltage control. Now reset the control midway between the minimum setting to obtain proper cardiac triggering and the maximum point of the *R* wave. The periodic response of the inhibit output signal should resume. Proper cardiac triggering has been obtained.

- Voltage Threshold

  The manual threshold voltage level can also be adjusted by observing the voltage threshold output in a “what you see is what you get” fashion. First, reduce the inhibit delay and threshold voltage levels to their minimum values. Adjust the oscilloscope so that the baseline traces of channels 1 and 2 are coincident with zero external input. Adjust the gain control of both channels to the same value, either 0.5 V or 1.0 V per division. It is important to adjust the oscilloscope channels to the same gain or else this procedure incorrectly sets the threshold voltage.

  Observe the filtered electrocardiogram on channel 1 and the signal from the PGM-1000 receiver output jack marked THRESHOLD OUT. The threshold voltage signal should coincide with the baseline of the ECG signal. Increase the ECG threshold voltage, until the trace observed on channel 2 lies midway between the top of the baseline features and the maximum of the QRS complex, as observed in the ECG. Disconnect the threshold voltage output from channel 2 of the oscilloscope and begin to observe the inhibit output signal. This signal should respond in a periodic fashion as each QRS complex is detected. The response pattern should be the same as that described above for proper cardiac triggering.

Once proper cardiac triggering has been obtained by one of the methods described above, proceed to adjust the inhibit delay.

Adjusting the Inhibit Delay

If proper cardiac triggering has been obtained, the inhibit delay can be adjusted by observing the electrocardiogram and inhibit output signals on channels 1 and 2 of the oscilloscope, as illustrated in Figure 108.

With the inhibit delay set to its minimum value, the inhibit output should decrease from +5 V to 0 V for a period of 50 ms, every time a QRS complex is detected. In this state (shown in Figure 108), the PGM-1000 receiver supplies the spectrometer with a trigger pulse for every QRS complex that appears in the ECG. If the pulse is not desirable, increase the inhibit delay to reduce the triggering frequency.

Slowly adjust the inhibit delay control to increase the inhibit delay time while observing the oscilloscope traces. Allow a few heart beats to pass, between each adjustment. Carefully note the response of the inhibit output trace.

At first, increasing the inhibit control simply lengthens the period of time the inhibit delay spends at 0 V after R wave detection. As soon as the length of the inhibit delay period approaches the value of the heart period, the inhibit output signal appears to respond erratically. The erratic response is caused by natural variations in the heart rate. A further increase of the inhibit delay causes the erratic pattern to disappear and a new periodic response (shown in Figure 108) to appear.

The new response of the inhibit output signal appears as a level change from +5 V to 0 V as a QRS complex is detected in the ECG. This change is followed by a delay greater than

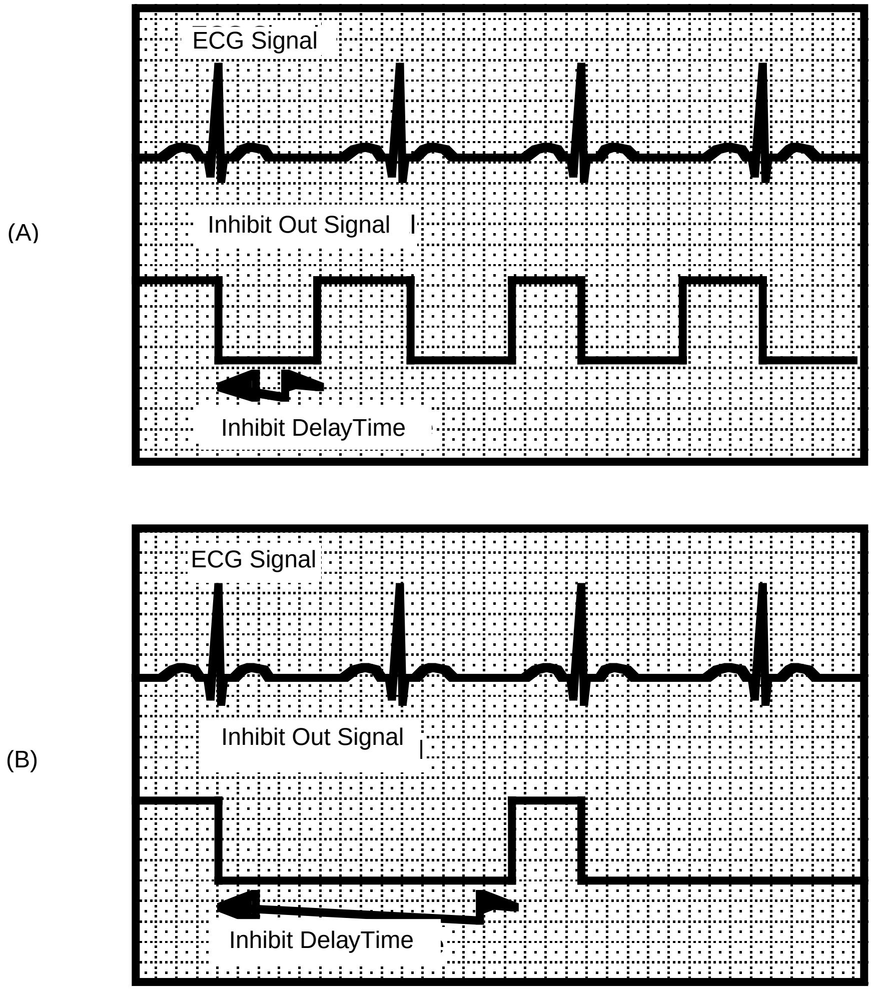


Figure 108. ECG and Inhibit Out: Trigger on (A) Each Heart Beat, (B) Every Other Beat

one heart period, in which the inhibit output signal is held at 0 V. During this interval, a second QRS complex appears in the ECG. The inhibit output then returns to the +5 V level in the second heart period. In this state, the PGM receiver outputs a trigger pulse for every second QRS complex detected in the ECG.

Increasing the value of the inhibit delay progressively reduces the triggering frequency. Each time the inhibit delay approaches an integer number of heart periods, the inhibit output makes a transition to erratic behavior, because of normal variations in the heart rate. To prevent erratic triggering, increase or decrease the inhibit delay.

Obtaining Images

Cardiac gated images can be obtained with most of the standard imaging pulse sequences. The operation of each sequence and its compatibility with gating operation is described in the manual *VNMR User Programming*. The slice profile projection modes of all sequences operate exclusively in the nongated mode.

Gating is usually activated through the parameter `ticks`. The value of `ticks` is the number of trigger pulses the system detects before proceeding to carry out the current scan.

Using a value of `ticks` greater than 0 provides a gated image. A value of `ticks` greater than 1 reduces the effective triggering frequency by a factor of `1/ticks`. Generally, it is better to use the inhibit delay feature of the PGM-1000, because this feature provides protection against false triggering and leads to a more stable triggering frequency.

The pulse sequence statement used to control gating, `xgate`, is inserted into sequence codes just prior to the "active" portion of the sequence, usually after the `d1` delay. With this placement of the gating statement, the sequence acts directly after the desired number of gating pulses have been counted off by the acquisition system.

An auxiliary delay parameter `hold` is provided to adjust the timing after the sequence triggers. This delay can be used obtain images at different phases of motion. The value of `hold` can be varied from zero to the value of the heart period.

Experiments that operate in the multislice mode trigger at the beginning of the sequence used to obtain the first slice. Subsequent slices are then run at a constant rate. The result is that all images are synchronized to the physiological trigger, but different slices are obtained at different points of the cardiac cycle.

A second auxiliary delay, `rcvry`, is provided before the gating statement for use in the multislice mode, where the `d1` delay controls sequence to sequence repetition. The `rcvry` delay is executed once before the sequence used to collect the first slice. The value of `rcvry` is chosen to allow the ECG to recover from the disturbance caused by the multislice sequence cascade.

The quality of gated images improves at short values of the echo time (`te`) and for higher numbers of averages (`nt`).

Simple Gated Spin Echo Imaging

To perform simple gated spin echo imaging, select the shorter sequence, which provides a spin echo imaging sequence compatible with short TE values. Select a TE value of 15 ms.

Obtain an initial scout image in the sagittal plane (`orient='zyx'`) along the center plane of the magnet. This plane should correspond to the central plane through the subject. In order to obtain this image in the gated mode, set the value of the parameter `ticks` as `ticks=1`. Set the delays `rcvry` and `hold` to zero. Choose the value of `d1` so that it is greater than one heart period. Choose all other parameters as appropriate for a single-slice scout image.

Once the sagittal scout image has been obtained, slice positions for coronal or transverse images can be selected. The scout image should show a diastolic heart, located in the chest cavity above the liver. The position of the ventricles should be readily apparent.

Target images can be obtained in the desired plane by adjusting the parameters in the normal way. Images of the heart in the diastolic phase can be obtained with value of the `hold` delay, equal to zero or slightly less than one heart period. Using a setting of the heart period minus the P-to-R wave interval for the parameter `hold` allows images with the both the atria and the ventricles in the diastolic state to be obtained. Images of the heart in the systolic phase can be obtained by using a value of the `hold` delay equal to the R-to-T wave interval in the ECG signal.

Images of the heart throughout the cardiac cycle can be collected by acquiring images separately, rather than by arraying the `hold` parameter.

Multislice Spin Echo Imaging

Multislice images can be obtained similarly to single-slice images, except that the value of `d1` is set so as to control the sequence to sequence repetition time in the multislice cascade.

The value of the `rcvry` delay is set greater than one heart period to allow the ECG signal to recover. Use of the manual threshold for cardiac triggering is recommended.

9.4 Performance Specifications

The PGM-1000 is used to detect the cardiac signal of an animal. The output of the PGM-1000 can be used to trigger a spectrometer or any medical instrument. The preamplifier is nonmagnetic and is installed in the magnet bore. An optical link transmits the information to the PGM-1000 Receiver, where the gating signal is created. The fiber optic link isolates the receiver from the preamp for safety and to prevent ground loops. 50 to 500 beats per minute with signal levels between 0.1 mV and 5 mV can be detected. The signal is FM modulated on a 33-kHz main carrier. Table 19 lists the performance specifications.

Table 19. PGM-1000 Performance Specifications

Function	*Specification*
Signal detection	Nonmagnetic patient leads and clips Signal level: 0.1 mV to 5 mV ECG rate: 50 beats/minute to 500 beats/minute
Signal modulation	ECG main carrier: FM 33 kHz ±10% for 6 V battery Battery indicator subcarrier: FM 3 kHz ±10% for voltage less than 4 V
Cardiac signal conditioning	High-pass filter: 0.5, 1.5, 5.0 and 10 Hz Low-pass filter: 20, 40, 80 and 160 Hz Gain select: x1, x10 Polarity select: positive or negative
Signal transfer	Single fiber-optic cable
Gating	Threshold: manual or automatic (half of cardiac signal) Inhibit time: 0.05 s to 2.5 s, adjustable
Indicators	Receiver power on/off Link on (preamp operational) Preamp battery low (on preamp and receiver)
Outputs	ECG analog signal: filtered and unfiltered (±12 V range) ECG trigger: 1 ms active low pulse Inhibit time: active low Threshold (0 V to 12 V)
Input	External inhibit signal
Power	Preamplifier: 6 V, 1.4 mA typical, battery operated Battery life: 150 h with Polaroid P100, 1000 h with Power-dex VP/6/1400 Receiver: 115 Vac, 50/60 Hz, switchable to 220 Vac on circuit board

Chapter 10. 2D and 3D Backprojection

Sections in this chapter:

This chapter shows how to acquire and reconstruct 2D and 3D NMR images based on the backprojection (BP) or projection reconstruction. The acquisition allows slice select and volume imaging sequences in 2D and 3D. The reconstruction of the acquired data covers the 2D and 3D case.

10.1 Installation

Note: Before running the BP software, make sure the imaging module is installed.

BP imaging software is included on the standard VNMR 5.3 installation CD-ROM. Loading BP software is accomplished the same as other VNMR software except the BP software requires a password. Refer to the manual *VNMR and Solaris Software Installation* for detailed installation information.

The installation disk contains the following files:

`bp3d.c`
`bp3d.par`
`bp3d`
	Pulse sequence, parameter set, and macro, respectively, written in obliquing style, which support 2D and 3D BP image acquisition.

`bp2d.c`
`bp2d.par`
`bp2d`
	Pulse sequence, parameter set, and macro, respectively, which support obliquing 2D slice select spin-echo BP image acquisition.

`bp_image.c`
`bp_image.par`
`bp_image`
`bp_setup`
	Pulse sequence, parameter set, and supporting macros, respectively, written in the original microimaging style, which support 2D and 3D BP image acquisition along with the selected NMR weighting T_1 (saturation recovery and inversion recovery), $T_{1\rho}$, and T_2.

`bp_reco`	Macro that executes the reconstruction of a 2D or 3D data set.
`bp_2d`	Program that performs the 2D reconstruction. Typical reconstruction time (based on a SPARCstation 2) is 2 seconds for a 256×256 from 128 projection.

`bp_3d`	Program that performs the 3D reconstruction. Typical reconstruction time (based on a SPARCstation 2) is 2 minutes for a $128 \times 128 \times 128$ from 64×64 projections, and 20 minutes for a $256 \times 256 \times 256$ from 128×128 projections.
`bp_mc`	Program that performs a magnitude calculation and is used prior to the program `bp_2d` or `bp_3d`.
`bp_sort`	Program that shuffles the projections obtained using an arrayed parameter in the order required by the `bp_3d` program.

Be aware that 3D BP image data sets may require up to 70 Mbytes of hard-disk space during acquisition and up to 100 Mbytes during the reconstruction.

10.2 Backprojection Image Generation

Figure 109 depicts the basic approach for BP image generation.

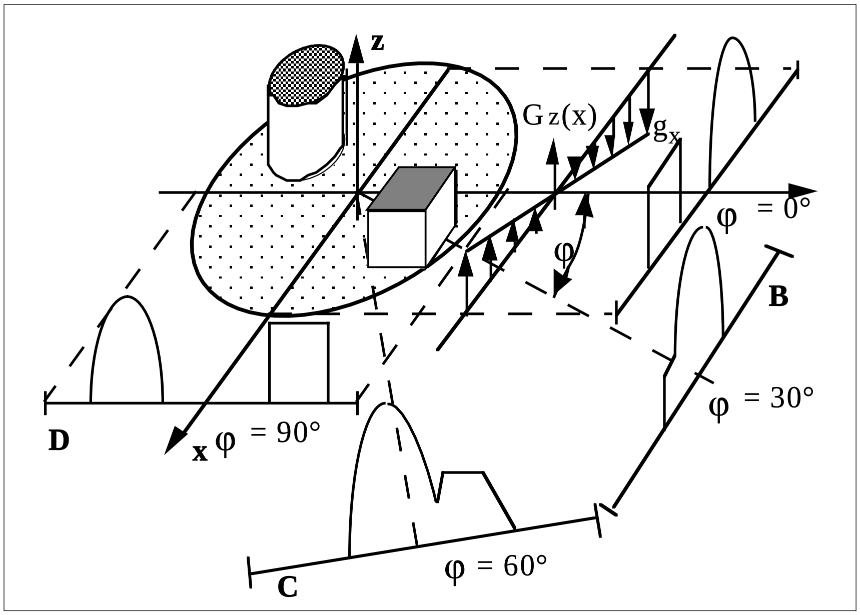


Figure 109. Image Generation Using Backprojection

Imagine a slice with a cylinder and a cube. Applying a field gradient Gz(x) along the x-axis (case A) results in a spatial one-dimensional field dependence $Bz = B_0 + x\ Gz(x)$ along the probe. Excitation of the probe with a short, non-selective rf pulse gives rise to a signal both from the cylinder and the cube. The different resonance frequencies of the cylinder and the cube (due to the applied gradient) result after Fourier transform in a profile exhibiting the cube and the cylinder. So far, a mapping of the 2D object to a 1D profile has been achieved. Note that the profile's intensities are determined by the line integrals perpendicular to the gradient direction.

To obtain a 2D image of the object, the direction of the gradient is changed (case B, C, and D). In comparing case A and D, it is obvious that the position of the cube and the cylinder in the profile have changed. By taking a series of angular projections over a range from 0° to 180°, the two dimensions of the object are mapped to the one dimension of the profile and the angular dependency.

A mathematical algorithm, named *projection reconstruction*, allows reconstruction of the 2D object from this series of angular projections. The BP package relies on an efficient implementation of this algorithm to provide short reconstruction times. Image generation can be performed not only in 2D but also in 3D.

10.3 Getting Started

This section describes the steps for setting up, acquiring, and reconstructing an image by using BP. A simple 2D slice select experiment is used in the example.

Retrieving a Parameter Set

Start with the following steps:

1. Verify that there is a sample in the probe and that the probe has been tuned, shimmed, and ready for experiments.
2. When you are ready to take a measurement, retrieve the parameter set by entering the name of the pulse sequence. In this example, to use the `bp2d` pulse sequence; enter **`bp2d`** to load the parameters.

   Figure 110 shows a typical display of `bp2d` parameters.

```
     NUCLEUS              RF PULSES            GRADIENTS            FIELD OF VIEW
tn              H1   rfcoil         tcoil  gcoil           main  orient          sag
sfrq       300.044                         pilot              y  lro            5.00
resto            0   p1            4000.0                        pro               0
                     p1pat           sinc  gro            1.525
   ACQUISITION       tpwr1             24  gpe                0   SLICE SELECTION
sw         32467.5                         gss            1.304  ns                1
at           0.002   p2            4000.0                        thk            2.00
np             128   p2pat           sinc                        pss               0
nv              64   tpwr2             30
nt               1                                                    SPECIAL
dp               y                                               phi2            180
                                                                 theta2            0
      DELAYS
tr          0.5000
te          0.0300
tspoil      0.0010
```

Figure 110. Parameter Set for bp2d

Setting Parameters for Acquisition

The experiment setup is basically the same as for a standard imaging experiment such as SEMS. Refer to Chapter 1, “First Steps: Making an Image,” for more information on setting up for an imaging experiment.

1. Set the `rfcoil` parameter to the correct value. Check that the `gcoil` parameter is correctly set.
2. Check that the pulse lengths (`p1` and `pw`), repetition and echo times (`tr` and `te`), and the transmitter offset resonance (`resto`) are appropriately set.
3. Set `lro` (length of readout, in cm) and `pss` (position of slice select, in cm) to the desired length and position. BP images are square images.

4. Set `np` and `nv`. The parameter `np` is the number of points in the readout projection Remember that `np` also determines the data size of the final image. `nv` is the number of projections to take, which determines acquisition time and image resolution.
5. Enter **`imprep`**. This macro uses the `rfcoil` and `gcoil` parameters to appropriately set the rf powers and gradient strengths.
6. Set `phi2` to 180 or 360, depending on whether a 180° or 360° rotation is desired when acquiring data. This is the only BP-specific parameter that needs to be set.

Taking a Measurement

You are ready to make a measurement.

1. Look at a profile of the image before acquiring the full image. In this case, set **`nv=0`**.
2. Enter **`go`** to start the measurement. When the acquisition is complete, enter **`ft`** to Fourier transform the data. Figure 111 shows a projection profile.
3. If the profile is acceptable, set `nv` to the desired number of projections and enter **`go`**.

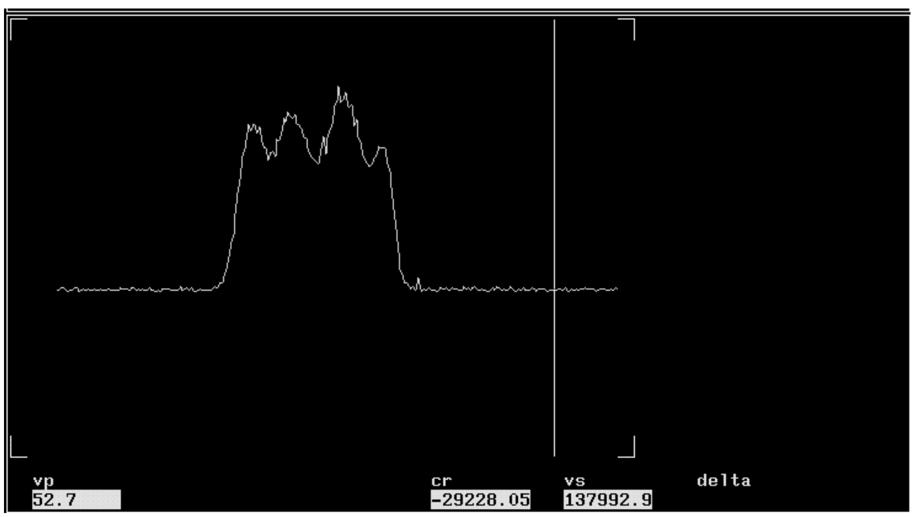


Figure 111. Profile of Fourier Transform of One Projection

Running Reconstruction

Reconstruction involves a Fourier transform followed by the macro `bp_reco`.

1. Enter **`ft`** to execute a Fourier transform.

   A counter in the upper right of the screen counts for all projections taken (`nv` times).
2. Enter **`bp_reco`** to start the reconstruction process.

   Messages appear for monitoring the status of the reconstruction (The following list shows only the most important messages):
   - `Magnitude calculation is running`. If an error occurs in this step, transform the data again and start the reconstruction.
   - `2D BP is running`
   - `2D BP is finished`

3. At the end of reconstruction process for a 2D dataset, the first (or only slice) is copied into the `data` and `phasefile` files in `expn/datdir`. This slice is also displayed in the VNMR graphics window.

   The single or multislice data is also reconstructed into Flexible Data Format (FDF) files for viewing by ImageBrowser. These files are put in `expn/datdir` with the names `bp2d000.fdf`, `bp2d001.fdf`,`... bp2dnnn.fdf`.

10.4 Routine Usage

This section describes the functionality provided by the BP imaging package and includes an overview of the NMR excitation schemes implemented with the package.

NMR Excitation Schemes

The BP package provides a variety of different NMR excitation schemes (slice and volume) and weighting of the signal obtained with NMR parameters ($T2$, $T1$, or $T1_{\rho}$, etc.). Table 20 lists the schemes implemented.

Table 20. Implemented NMR Excitation Schemes

Probe Excitation	*Sequence*	*NMR Weighting Parameters* *Preparation*	*Imaging*	*BP Imaging Result*
slice	bp2d	-	T2	one or more image slices
volume/slice	bp_image	T_1(sr,ir,aps)	T2	one image slice
volume/slice	bp_image	T1rho	T2	one image slice
volume	bp3d	-	T2	one image slice
volume	bp_image	T_1(sr,ir,aps)	T2	one image slice
volume	bp_image'	T1rho	T2	one image slice
volume	bp3d	-	T2	(volume)
volume	bp_image	T_1(sr,ir,aps)	T2	(volume)
volume	bp_image	T1rho	T2	(volume)

T_2 weighting of the NMR signal (a spin echo in the imaging case) is achieved by setting the echo time, `te`, in the imaging phase. T_1 and $T_{1\rho}$ weighting are performed in a preparation phase prior to the imaging phase. In the case of T_1 weighting, three different excitations are supported: saturation recovery (`sr`), inversion recovery (`ir`), and aperiodic saturation recovery (`aps`).

Reconstruction results in one or more image slices or a volume. The acquisition and reconstruction of a series of slices or volume takes considerably longer than acquisition and reconstruction of a single slice.

Pulse Sequences

The backprojection package has three pulse sequences:

- Sequence `bp2d` supports 2D slice select imaging, and has an interface similar to the imaging module interface used to support oblique imaging.

- Sequence bp3d sequence supports 2D and 3D volume imaging, and also has an interface similar to the imaging module interface used to support oblique imaging.
- Sequence bp_image supports 2d slice select, 2D volume, and 3D volume imaging, and has an interface similar to the microimaging module interface.

Table 21 provides data for each imaging method.

Table 21. Estimated Acquisition and Reconstruction Times

Method	*np*	*Acquisition Time*	*Reconstruction Time*	*Image Matrix*
2D slice	128	32 × (TE + TR)	< 1 second	64 × 64
2D slice'	256	64 × (TE + TR)	2 seconds	128 × 128
2D slice	512	128 × (TE + TR)	5 seconds	256 × 256
2D vol	128	32 × (TE + TR)	< 1 second	64 × 64
2D vol	256	64 × (TE + TR)	2 seconds	128 × 128
2D vol	512	128 × (TE + TR)	5 seconds	256 × 256
3D vol	128	1024 × (TE + TR)	35 seconds	64 × 64 × 64
3D vol	256	4096 × (TE + TR)	2 minutes	128 × 128 × 128
3D vol	512	16384 × (TE + TR)	20 minutes	256 × 256 × 256

Acquisition and Reconstruction with Sequences bp2d and bp3d

When setting up for an acquisition with pulse sequences bp2d and bp3d, the standard imaging method should be used.

Setting Up for Acquisition

To set up for dp2d and dp3d, check the following settings and then run macro imprep:

1. Make sure rfcoil and gcoil have been defined.
2. Set any desired pulse lengths. For volume imaging using bp3d, have pulse lengths as short as possible in order to irradiate as large of volume as possible. Some versions of the sequence should be run with square (nonselective) pulses.
3. Set the transmitter offset resonance.
4. Set te and tr. If te is large enough, the pulse sequence puts the spin echo in the middle of the acquisition time. Otherwise, the spin echo will appear in the left, shifted. Note that reconstruction artifacts might appear if the spin echo appears too left shifted. Setting tr is a compromise between total measurement time and full T_1 relaxation in the case of pure T_2 weighting, as well as for sr and ir T_1 weighting.
5. If using dp2d, set lro (image size) and pss (position of slice selected).
6. Set trans, sag, and cor (orientation parameters). The angles psi, phi, and theta can also be set for an oblique orientation.
7. Set np for the number of points to acquire. np determines the size of the image.
8. Set nv for the number of projections to acquire for 2D. Also set nv2 for 3D.
9. Set phi2 and also theta2 for 3D. These values select between a 180° or a 360° angular span of the projections taken. Usually, the 180° span is taken, because the projections obtained at 0° are identical to the centrally mirrored projections from

180°. However, in slice-selective excitations and cases of B_0 shift due to gradient switching, the image quality can be improved by taking projections from the full 360° span.

10. Enter **`imprep`**, which calculates rf strengths, gradient strengths, and timing.

Starting the Measurement

The following steps perform the measurement for sequences `dp2d` and `dp3d`:

1. Enter **`go`** to start the acquisition.
2. Check the spin echo signal by displaying it with `df`.

   If the signal amplitude is too high, decrease the gain with `gain=lower_value`.

You can also look at projections during acquisition by entering **`ft`** and then **`ds`**.

Performing the Fourier Transform

To obtain profiles from the projections taken, perform a Fourier transform. You may use an unweighted or weighted transform.

- For an unweighted transform, enter **`ft`**.
- For a weighted transform, weighting is determined by the desired pixel resolution and the available signal-to-noise. To set the weighting, enter **`wti`** and `then` **`wft`**. Figure 112 shows a typical display. If the center of your spin echo is left shifted, move the center of the weighting function to the same position.

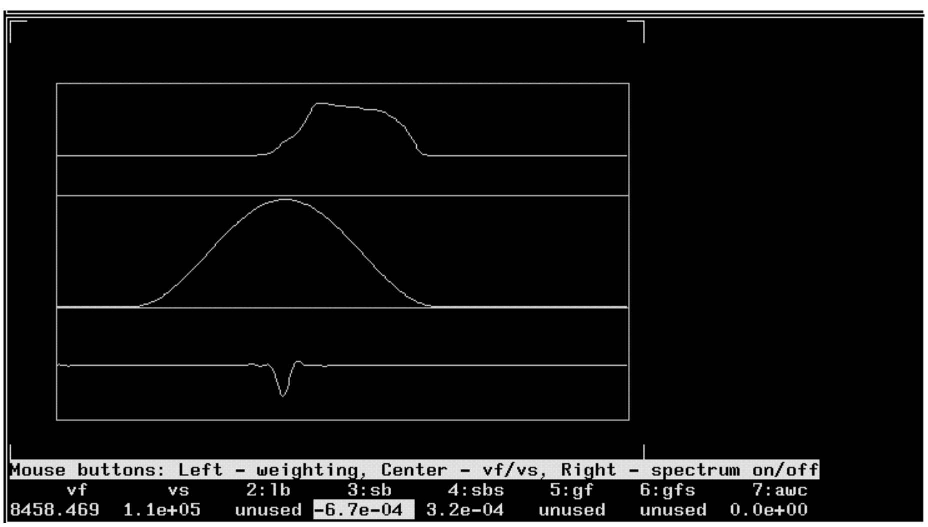


Figure 112. Setting the Weighting

Use the following guidelines to adjust the weighting: (1) Choose the width of the weighting function to be at least 5 to 10 times broader than the width of the echo signal, and (2) Make sure the weighting function has decreased to nearly zero at the left and right side of the scan. If it is truncated with a large nonzero value, artifacts in the reconstruction will appear.

An example of the effect of the weighting appears in Figure 113, which shows a comparison of an unweighted and a weighted FT. It is obvious that the course of the profile is smoother after the weighted transform.

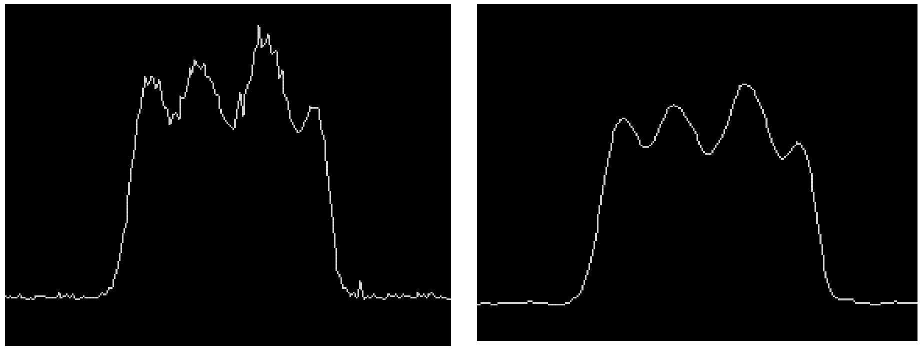


Figure 113. Unweighted and Weighted Fourier Transform

Performing Reconstruction

The macro `bp_reco` takes care of the reconstruction process. For the duration of the reconstruction, refer to Table 21.

1. Enter **`bp_reco`** to start the reconstruction process.
2. When running a 3D reconstruction, a text file appears with settings that will be used for the reconstruction. You can modify the text file at this time if you want to change any of the default settings. In any case, you must quit or exit the editing window in order for the reconstruction to proceed.

   In the 2D case, the window does not appear.
3. The following messages appear, allowing you to monitor the reconstruction process.
   ```
   Magnitude calculation is running
   Profile generation finished
   2D/3D BP is running
   2D/3D BP is finished
   ```

See "BP Macros and Programs Details," page 249, for a detailed description of the individual settings passed between the program constituting the reconstruction.

Sometimes errors might appear in the magnitude calculation section, for example:

```
bp_mc: can't read bhead
```

This error generally results when the initial Fourier transform has been performed on only one projection or a subset of the total projections. To fix the problem, enter **`ft`** or **`wft`** again and rerun **`bp_reco`**.

Displaying the Dataset

At the end of the reconstruction process, the data is written out for display:

- For a 2D dataset, the first slice (or only slice) is copied into the `data` and `phasefile` files in `expn/datdir` so that the slice can be viewed by VNMR. Also, the single or multislice data is reconstructed into FDF files for viewing by ImageBrowser. These files are also located in `expn/datdir` with the names `<seqfile>000.fdf`, `<seqfil>001.fdf,... <seqfile>nnn.fdf`.
- For a 3D dataset, the data is written out to a FDF file in `expn/datdir` named `<seqfile>.fdf`. The display program `disp3d` is also started with the data, so you can immediately view the 3D dataset. This 3D dataset can also be viewed slice by slice by using ImageBrowser.

disp Program

The `disp` program displays a 3D FDF file or a raw 8-bit 3D data file with no header. After data has been loaded, a 3D volume appears in the display window. The initial appearance of the 3D volume is as if it was viewed from the front.

To change the size, position, orientation, and slice of the 3D volume, do the following procedures:

- Adjust the size of the displayed image by using the *left* button of the mouse to increase or decrease the value on the Zoom slider. For FDF format data, the image is initially scaled to actual size, or, if that would be impractical, it is scaled up or down by a power of two. The zoom field gives the displayed scale as a percentage of actual size.
- Adjust the brightness and contrast of the display with the Contrast slider and the Vscale type-in field. The contrast adjusts the colormap to optimize the display of the 8-bit data. The Vscale value is used only for FDF data with a word size greater than 8 bits. The data are multiplied by the factor `255*vscale` before being truncated to 8 bits. (If `vscale=1`, a data value of 1.0 scales to maximum intensity.)
- Adjust the position of the 3D volume by using the *middle* button of the mouse and dragging it to the desired position inside the display panel.
- Adjust the orientation of the 3D image by holding down the *left* button of the mouse while moving the cursor inside the display panel. The image can also be rotated about the Z axis (perpendicular to the screen) by moving the Rotate slider in the control panel. The Snap button rotates the image to the nearest orientation that makes all the orientation angles multiples of 15 degrees.
- Adjust the displayed slice of the 3D image by using the face selector and the Slice plane slider. The plane selector selects one face of the data cube, and the slider moves the active slice through the volume. If the 2D display selector is On, each slice is displayed in the lower left corner as the slice position slider moves through the volume.

The `disp3d` display window also includes the following features:

- The 3D Display selector selects viewing the 3D volume in image mode, image plus wire frame, or wire-frame-only mode.
- You can adjust the background color of the display panel (through the Bkgnd entry point) by controlling the levels of the red, green, and blue channels of the color display. Examples of color settings are 255 255 255 for white, 0 0 0 for black, and 128 128 128 for gray.

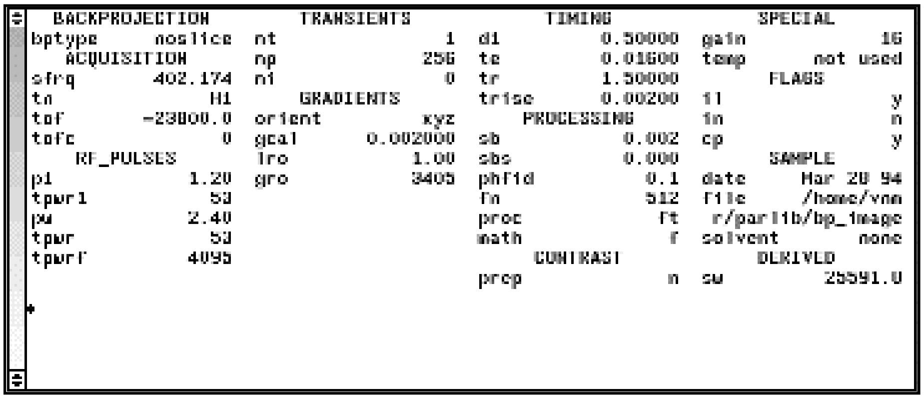
Acquisition and Reconstruction with Sequence bp_image

This section describes how to use the `bp_image` pulse sequence, which uses an older style of imaging pulse sequence development. `bp_image` provides a number of NMR weighting and excitation schemes.

Loading Parameters

Parameters for the `bp_image.c` pulse sequence are located in the `bp_image.par` directory. Load the parameters by entering **`bp_image`**.

Figure 114 shows a typical display of reference parameters.



BACKPROJECTION		TRANSIENTS		TIMING		SPECIAL	
bptype	noslice	nt	1	d1	0.50000	gain	16
ACQUISITION		np	256	te	0.01600	temp	not used
sfrq	402.174	ni	0	tr	1.50000	FLAGS	
tn	H1	GRADIENTS		trise	0.00200	il	y
tof	-23000.0	orient	xyz	PROCESSING		in	n
tofc	0	gcal	0.002000	sb	0.002	cp	y
RF_PULSES		lro	1.00	sbs	0.000	SAMPLE	
p1	1.20	gro	3405	phfid	0.1	date	Mar 20 94
tpwr1	53			fn	512	file	/home/vnm
pw	2.40			proc	ft		r/parlib/bp_image
tpwr	53			math	f	solvent	none
tpwrf	4095			CONTRAST		DERIVED	
				prep	n	sw	25591.0

Figure 114. Parameters for Sequence dp_image

Setting System-Specific Parameters

Some reference parameters differ depending on the system configuration. Perform the following steps to make sure these parameters are correct for your system.

1. Check that `sfrq` has the correct spectrometer frequency (300, 400, etc.) for your system.
2. For slice-selective imaging, use a shaped pulse. For volume imaging, use a square, or hard, pulse.
3. Check that `tpwr1` is set to an appropriate transmitter power for a 90° pulse and that `p1` is set to the duration of the 90° pulse.
4. Check that `tpwr` is set to an appropriate transmitter power for a 180° pulse and that `pw` is set to the duration of the 180° pulse.
5. Check that the gradient strength is calibrated. See the appendix, “Commands, Macros, and Parameters,” for guidelines for using the macro `setgcal` to check gradient strength calibration.

Setting On-Resonance

BP imaging requires the on-resonance condition to ensure an identical center in all projections obtained for one image. To set on-resonance, perform the following steps.

1. Enter **`gro=0`** to disable gradients.
2. Enter **`go`** to acquire one scan. You should see a signal.

   If no signal is seen, check `te` (echo time) and `gain` (receiver gain). To increase the signal, decrease `te` or `gain`. The echo may not be centered in the time domain.
3. Enter **`ft`** to Fourier transform the data, and then move the cursor on the line in the spectrum and enter `movetof` to set the spectrometer frequency to the cursor value. Your display should be similar to the display in Figure 115.

Setting BP Image Acquisition

The next step is to run the `bp_setup` macro. You should now set up the BP imaging sequence according to your needs as follows.

1. Enter **`bp_setup`** to run the macro. The following questions are asked:

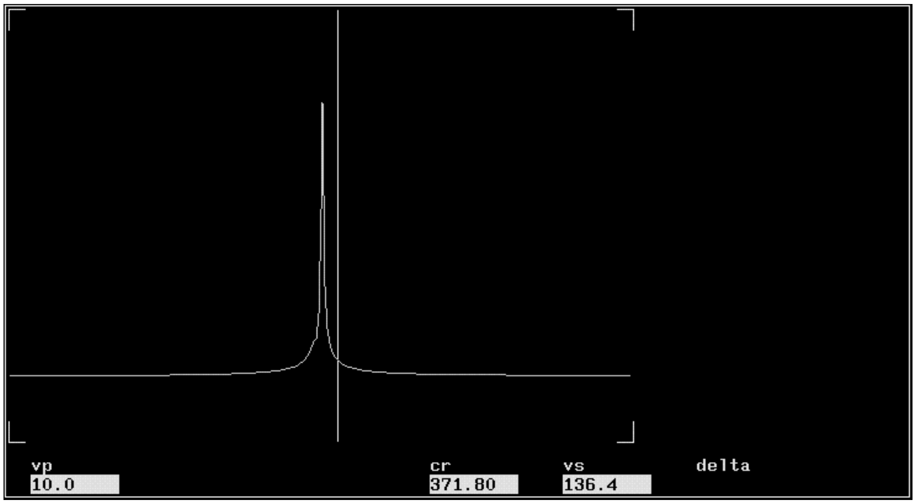


Figure 115. On-Resonance Condition

a. `BP type (bp3d, bp2d, bp2ds)?`

According to Table 20, you may select volume excitation schemes (`bp3d` or `bp2d`) or the slice-selective excitations scheme (`bp2ds`).

b. `Preparation (none, sr, ir, aps, t1r)?`

Table 20 summarizes the selections available in the preparation phase. The selection `none` disables any excitation in the preparation phase, thereby allowing only T_2 weighting. `sr`, `ir`, or `aps` result in T_1 weighting using saturation recovery, inversion recovery, or aperiodic saturation, respectively.

c. `Maximum diameter of probe (mm)?`

Imagine a sphere in the magnet center that completely contains the probe under investigation. Take the diameter of the sphere, increase it by roughly 20%, and take the resulting value as the diameter of the field of view (FOV) of your BP image or volume.

d. `Number of points in profile (np)?`

The number `np` refers to the number of points during acquisition (real plus imaginary values). Therefore, `np` is twice the number of points in the reconstructed image. For setting `np`, use a power of 2 (64, 128, 256, or 512). Table 21 lists the estimated acquisition and reconstruction times (in the table, TE is the spin echo time, TR includes the recovery time and preparation time required, and `np`/4 projections are assumed). Note that measurement and reconstruction time does not increase linearly with the increasing `np` for 3D data sets.

e. `Expected pixel resolution (Hz)?`

The pixel resolution, in Hz, refers to linewidth of the probe. For discrimination between two adjacent pixels having a Lorentzian lineshape on at least the 50% amplitude level, the pixel resolution has to be greater than or equal to the linewidth. This requirement can easily be met in biological samples. In polymers, usually only equality can be achieved In rigid materials, the maximum gradient results in a limitation. The macro `bp_setup` checks your value against the technical limitations internally.

f. `Angle phi (180 degree, 360 degree)?`

This option selects between a 180° or a 360° angular span of the projections taken. Usually, you take the 180° span because the projections obtained at 0° is identical to the centrally mirrored from 180 degree. However, in slice-selective excitations and cases of B_0 shift caused by gradient switching, the image quality can be improved by taking projections from the full 360° span.

g. `Angle theta (180 degree, 360 degree)?`

This option is only valid for 3D acquisition and reconstruction. It should be set to the same value as for the angle `phi`.

2. `bp_setup` checks your values for validity, computes sweep width and digitizer resolution, checks gradient strength (including an overrange test), and presets the spin echo time, `te`. The values obtained are printed out, similar to Figure 116.

```
---   READOUT SETTINGS   ---

field of view    = 15.0000    resolution = 0.05859
sweep width      =   51200    np/2       =     256
acquisition time = 0.00500    gro        =    7975
readout gradient= 7.9559 gauss/cm
```

Figure 116. Macro bp_setup Values Display

You can accept or reject these values from the message:

`Use these values? (y/n):`

3. Enter **y** to accept the values or `n` to reject the values.
4. Set the spin echo parameter `te` to the value you want.

If `te` is large enough, the pulse sequence puts the spin echo in the middle of the acquisition time. Otherwise, the spin echo appears in the left, shifted. Note that reconstruction artifacts might appear if the spin echo appears too left-shifted.

5. Set the recovery time parameter `tr` to the value you want.

In the case of pure T_2 weighting as well as for `sr` and `ir` T_1 weighting, setting `tr` is a compromise between total measurement time and full T_1 relaxation. For T_1 weighting using `aps`, `tr` can be set to the time value currently measured, because the `aps` sequence completely dephases the magnetization on its own.

Starting the Measurement

Enter **go** to start the measurement.

Other Excitation Schemes

The remainder of this section shows the use of pulse sequences for the different excitation schemes. Where applicable, further parameters to control the operation are described.

Volume-Based BP Acquisition

As indicated in Figure 117, each pulse sequence consists of a preparation phase (indicated by A) and the image acquisition phase (indicated by B).

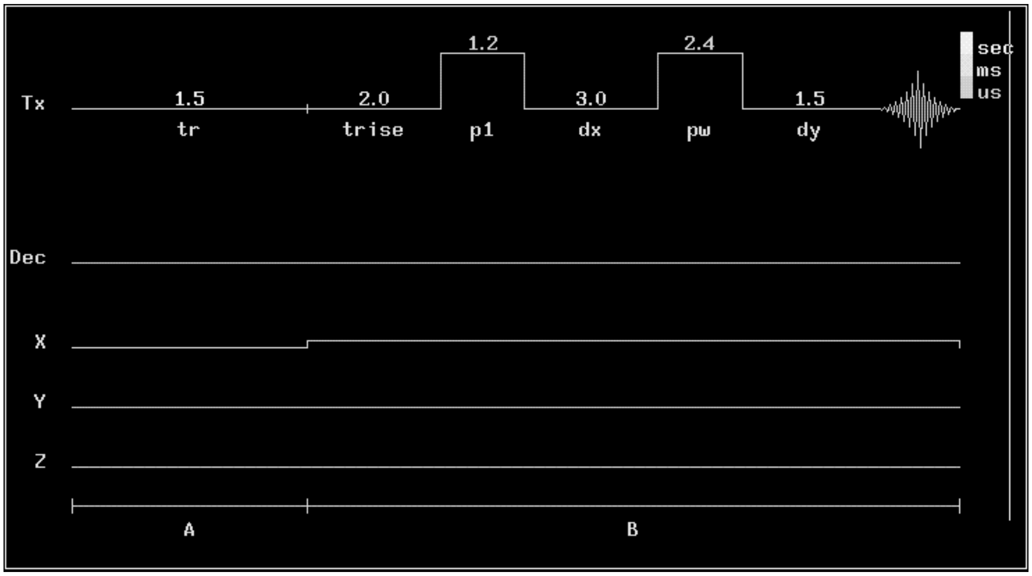


Figure 117. Phases: (A) Preparation and (B) Acquisition

The preparation phase A takes the recovery time, `tr`, and any NMR weighting applied with `sr`, `ir`, and `aps`. The acquisition phase B starts with a period of time (`trise`) covering the switching of the gradients. It continues with two rf pulses, usually a 90°-dx-180° sequence (selective or nonselective according to the selection `bp2ds` or `bp2d` and `bp3d`). The spin echo time, `te`, is determined by `dy` and the acquisition time.

In this type of acquisition, only hard pulses are used for excitation, thus taking the signal of the whole probe in each projection step. Depending on the available measurement time, signal-to-noise considerations, and the properties of the probe, a 2D (method `bp2d`) or 3D (method `bp3d`) image can be acquired.

In case of a 2D image acquisition, the reconstructed intensity in each pixel refers to the summed up intensities along a line perpendicular to the chosen image plane. This non-slice-selective approach results in a short measurement time for a 3D object and is useful in cases of poor signal to noise, or it can serve as a scout view.

In case of a 3D image acquisition, each voxel in the reconstructed volume (series of slices) refers to the signal obtained from the particular pixel position (x, y, z).

Both the 2D and 3D type of acquisition use the same pulse sequence.

T_2 Weighted 2D and 3D BP Pulse Sequence

The T_2 weighted pulse sequence is shown in Figure 118. The preparation phase A contains only the recovery time, `tr`. After phase A, the gradients are switched on and allowed to settle as set by `trise`. T_2 weighting is achieved during acquisition phase B by setting the spin echo time, `te`. If `te` is smaller than the sum of `dy` and half of the acquisition time, the echo occurs left-shifted.

T_1 Weighting Using Inversion Recovery or Saturation Recovery

T_1 weighting in the preparation phase A is achieved by a 90° pulse (saturation recovery, `sr`) or by a 180° pulse (inversion recovery, `ir`). The pulse is controlled by `pi` and `tpwri`.

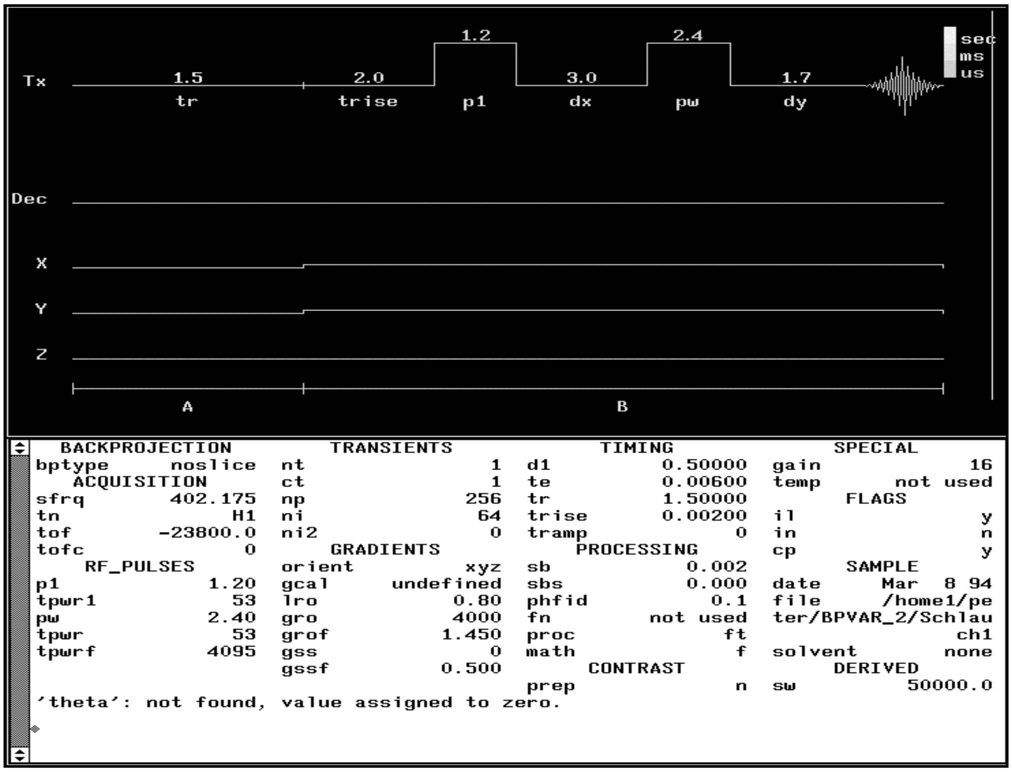


Figure 118. T_2 Weighted 2D and 3D Pulse Sequence

In acquisition phase B, set `te` to a small value in order to reduce T_2 weighting influence. Figure 119 shows an example of a T_1 weighting–preparation phase.

T_1 Weighting Using Aperiodic Saturation

Aperiodic saturation is achieved by a sequence of 90° pulses in the preparation phase. The time period between the pulses is continuously divided by two to achieve full dephasing corresponding to full saturation. The particular advantage of the `aps` sequence is the short measurement time, because there is no requirement on the initial state of magnetization prior to the `aps` sequence (`d1`) may be chosen quite small). Therefore, measurements of the points of the T_1 relaxation curve don't need a fully relaxed state requiring 3 to 5 times T_1 as a recovery time. The parameter `nsat` controls the number of pulses used in `aps`. The parameter `sat` controls the duration between the first pulse and second pulse. The parameters `pi` and `tpwri` control the pulse. Figure 120 shows an example of T_1 weighting using aperiodic saturation.

T1rho Weighting

$T_{1\text{rho}}$ weighting is achieved by a 90° pulse that flips the magnetization in the xy plane and a subsequent spin lock pulse `pj`, which phase is perpendicular to the 90° pulse. After the spin lock duration `pj`, the magnetization is flipped back in the z-direction and the standard imaging sequence follows. Between the 90° pulses and the spin lock pulse, a small delay (typically 4 µs) is necessary to allow for transmitter phase switching. Note that the spin lock pulse is in the range of milliseconds. Figure 121 shows an example of $T_{1\text{rho}}$ weighting.

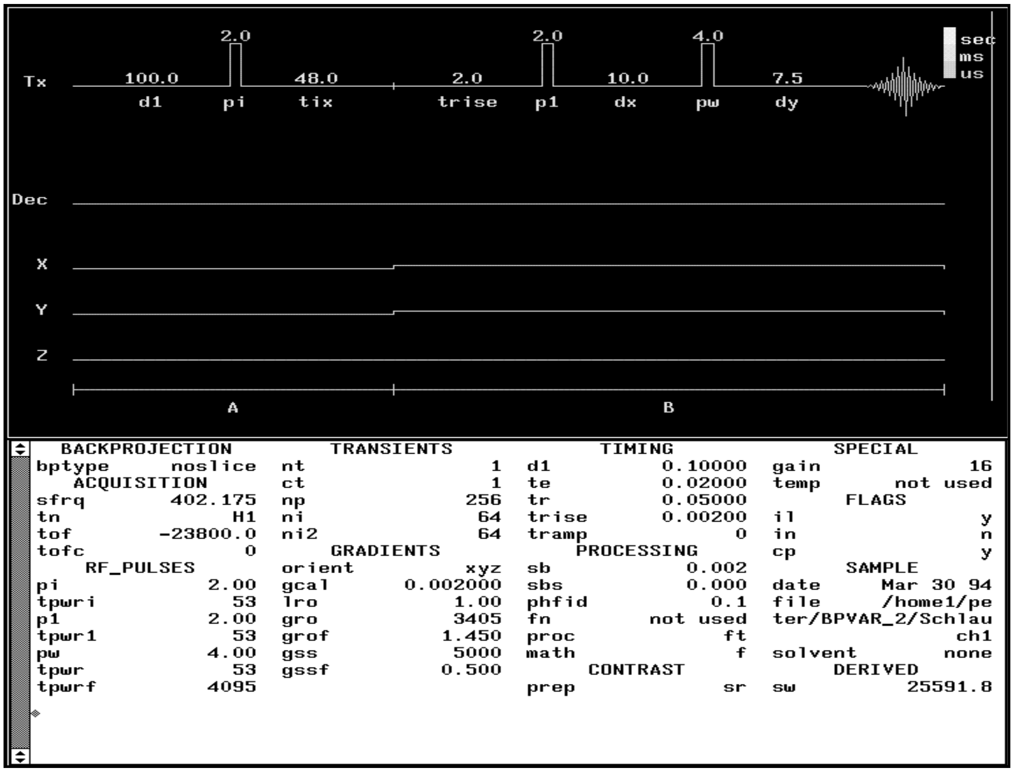


Figure 119. T_1 Weighting–Preparation Phase

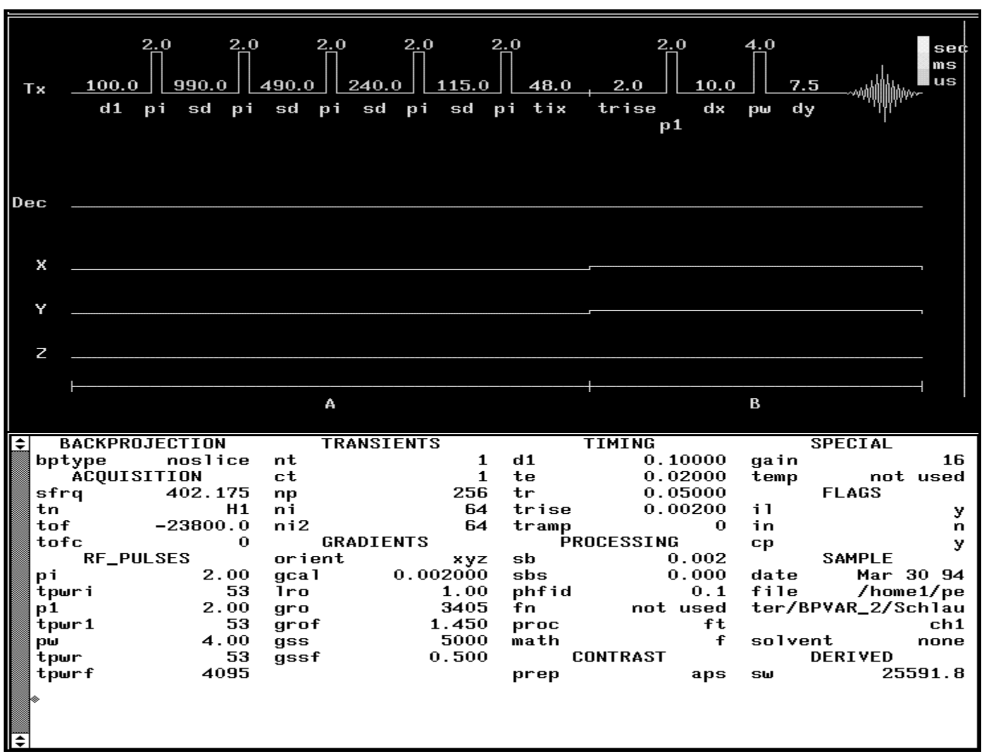


Figure 120. T_1 Weighting–aps Sequence

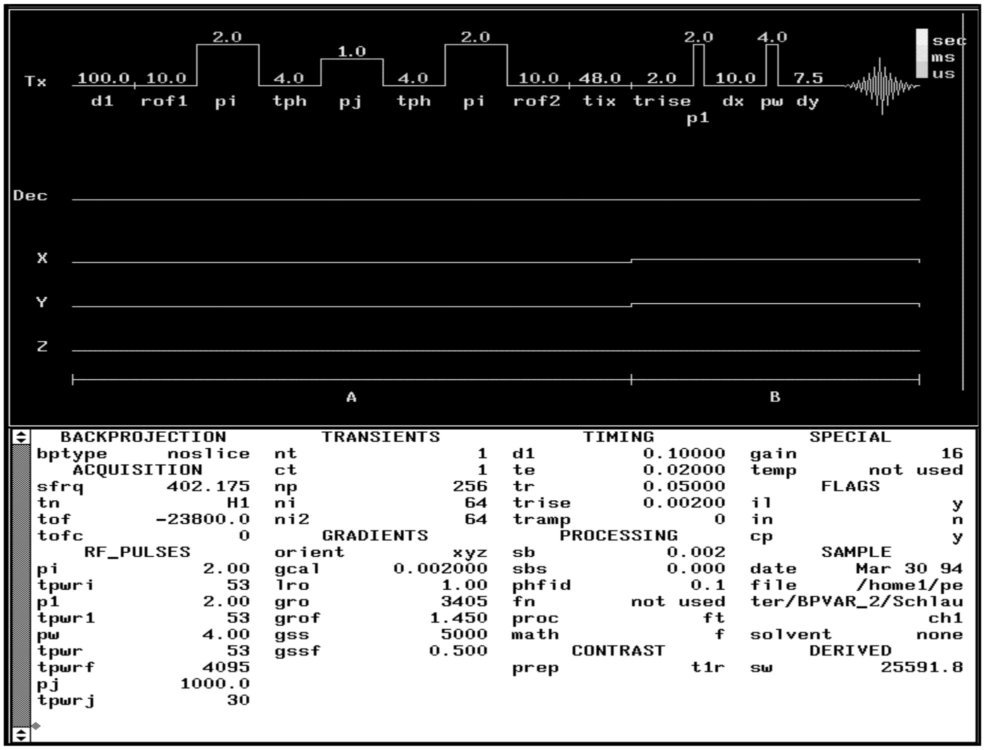


Figure 121. T_{1rho} Weighting

Slice-based BP Acquisition

In slice-based acquisition (`bp2ds`), soft pulses are used for imaging, thus selecting a slice. Any NMR weighting in the preparation phase is done with hard pulses, thereby not allowing multi-slice experiments. However, you may array any parameter to measure several slices according to the arrayed parameter. The `bp_2d` reconstruction is able to reconstruct these arrayed slices.

The reconstructed intensity in each pixel of the slice refers to the signal obtained from the particular pixel position (x, y).

The pulse program consists of a preparation phase A and acquisition phases B and C.

The preparation phase A takes the recovery time, `tr`, and any NMR weighting applied with `sr`, `ir`, and `aps`. The acquisition phase starts in B with a 90° slice-selective pulse (`p1`, `tpwr1`, and `p1pat`). In Figure 122, the pulse selects an xy plane using the z-gradient. After the pulse, the magnetization along the slice thickness is refocused (z-gradient) and dephased in the plane (x-, y-gradient). The 180° slice-selective pulse (`pw`, `tpwr`, or `pwpat`) inverts the magnetization in the selected slice and results in a spin echo in phase C. The slice profile is controlled by the pulse pattern (`pwpat` or `p1pat`) and the duration of the pulse (`p1` and `pw`). The position of the slice is set by the frequency offset to `sfrq` + `tof` of the selective pulses.

T_2 Weighted 2D Slice-Selective BP Pulse Sequence

The T_2 weighted pulse sequence is shown in Figure 123. The preparation phase A contains only the recovery time, `tr`. T_2 weighting is achieved during the phase C by setting the spin echo time, `te`. The spin echo might appear left shifted because of a time constraint imposed by setting `te` too small.

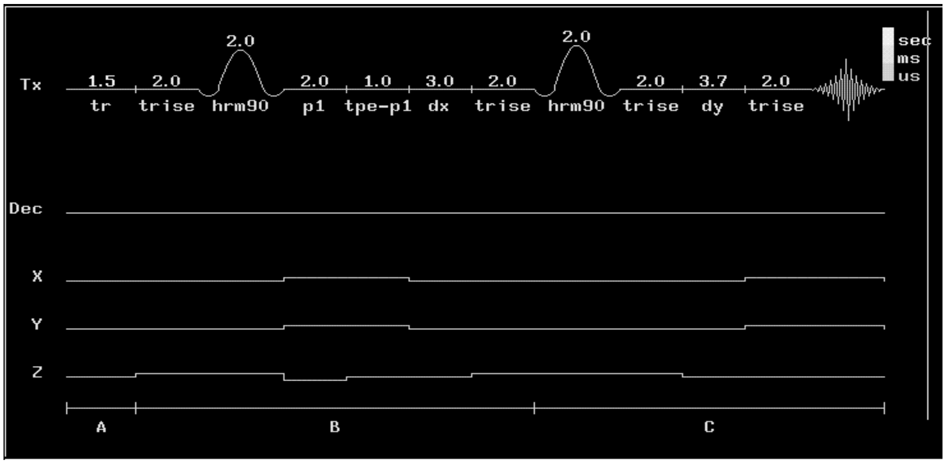


Figure 122. Slice-based BP Acquisition

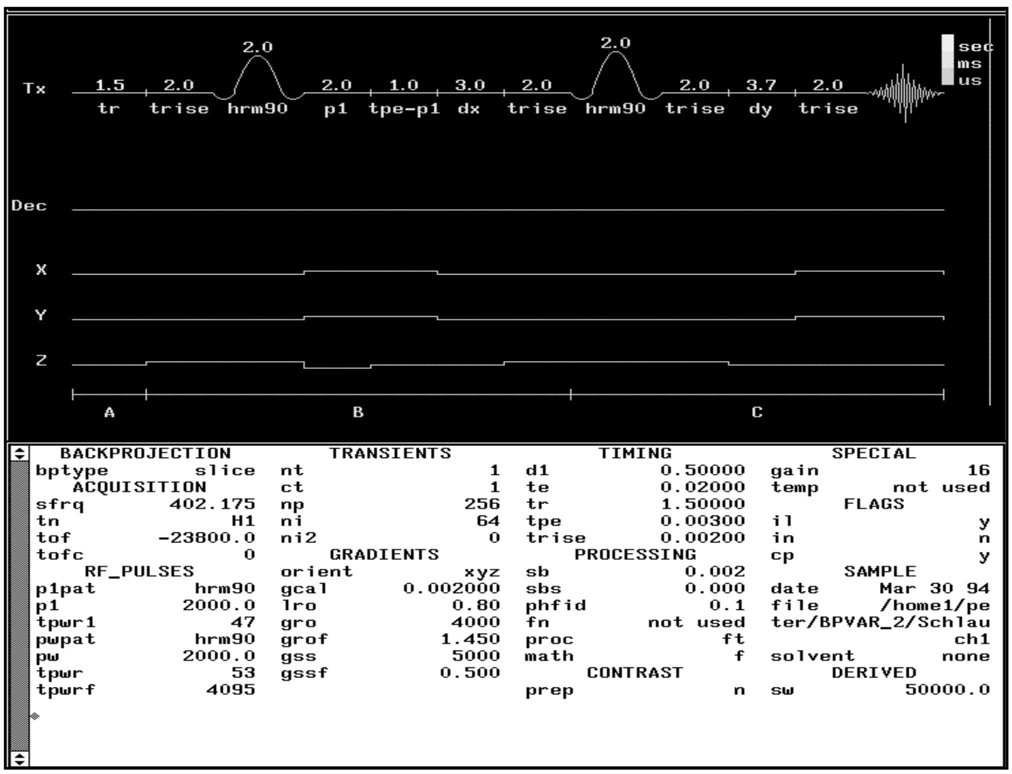


Figure 123. T_2 Weighted 2D Slice-Selective Pulse Sequence

T1 Weighting Using Inversion Recovery or Saturation Recovery

T_1 weighting in the preparation phase A is achieved by a 90° pulse (saturation recovery, `sr`) or by a 180° pulse (inversion recovery, `ir`). The pulse is controlled by `pi` and `tpwri`. In acquisition phases B and C, set `te` to a small value to reduce the T_2 weighting influence. Figure 124 shows an example of T1 weighting using `ir` or `sr`.

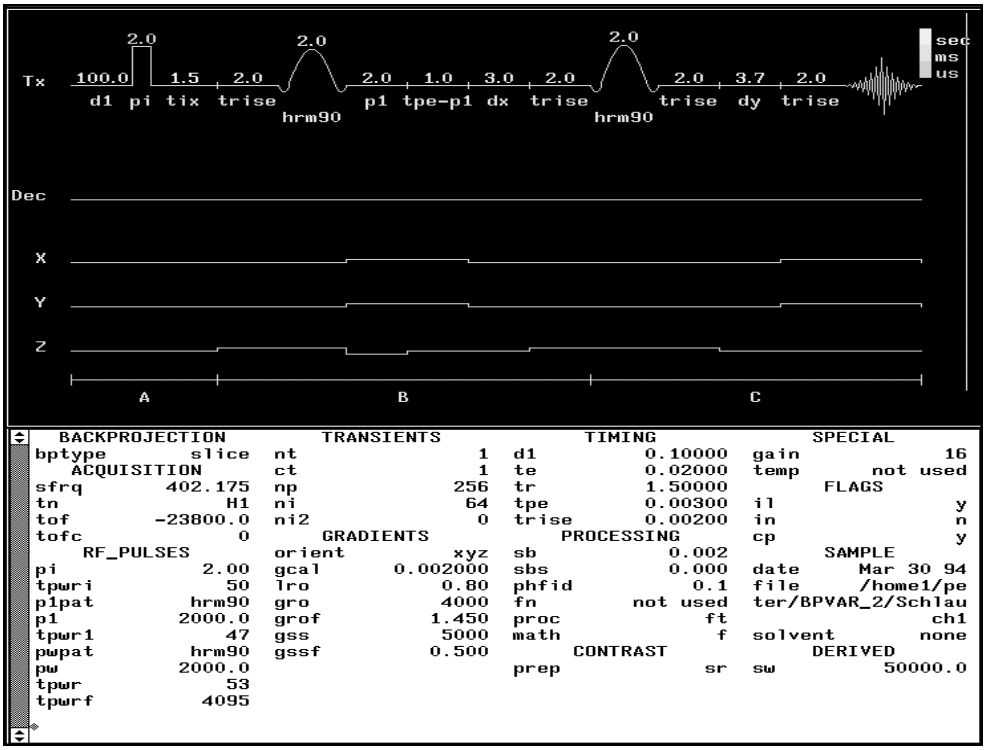


Figure 124. T_1 Weighting–Inversion or Saturation Recovery

T_1 Weighting Using Aperiodic Saturation

Aperiodic saturation is achieved by a sequence of 90° pulses in the preparation phase. The time period between the pulses is continuously divided by two to achieve full dephasing that corresponds to full saturation. The particular advantage of the `aps` sequence is the short measurement time, because there is no requirement on the initial state of magnetization prior to the `aps` sequence. Therefore, measurements of the points of the T_1 relaxation curve don't need a fully relaxed state requiring 3 to 5 times T_1 as a recovery time. The parameter `nsat` controls the number of pulses used in `aps`. The parameter `sat` controls the duration between the first pulse and second pulse. The parameters `pi` and `tpwri` control the pulse. Figure 125 shows an example of T_1 weighting using aperiodic saturation.

T_{1rho} Weighting

The $T_{1\text{rho}}$ weighting is achieved by a 90° pulse that flips the magnetization in the xy plane and a subsequent spin lock pulse, `pj`, which phase is perpendicular to the 90° pulse. After the spin lock duration `pj`, the magnetization is flipped back in the z-direction and the standard imaging sequence follows. Between the 90° pulses and the spin lock pulse, a small delay (typically 4 µs) is necessary to allow for transmitter phase switching. Note that the spin lock pulse is in the range of milliseconds.

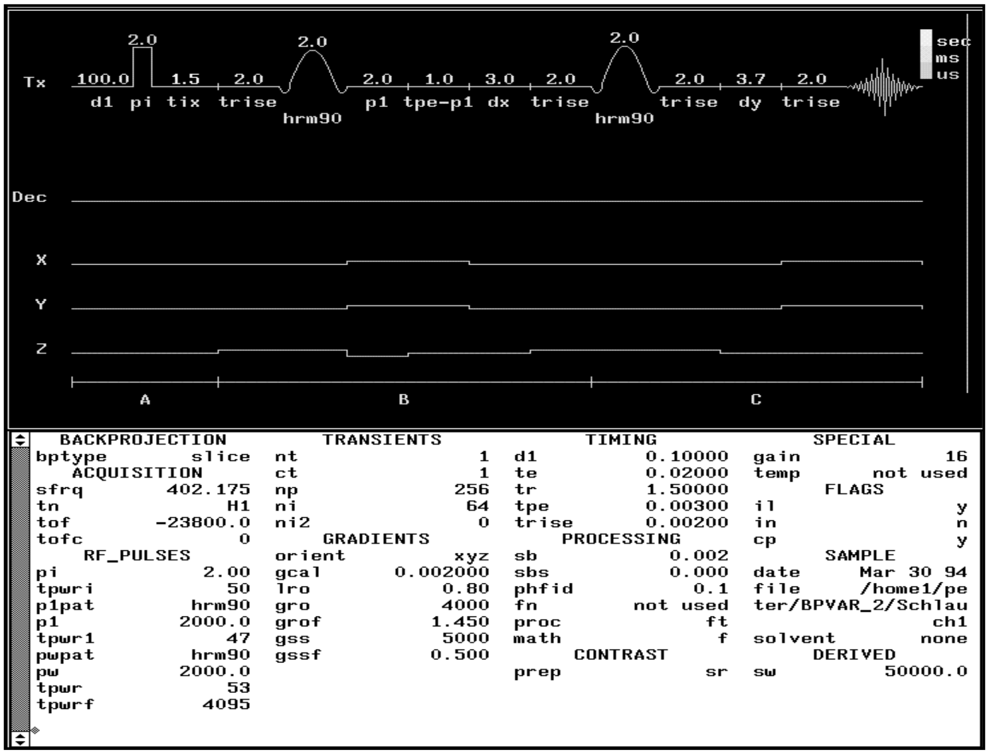


Figure 125. T_1 Weighting–Inversion or Saturation Recovery

Parameters in BP Package

The following parameters are related to the BP package:

`tofc`	Transmitter frequency offset for slice-selective excitation.
`gro`	Readout gradient.
`grof`	Factor for fine tuning of the readout gradient compensation.
`gss`	Slice gradient.
`gssf`	Factor for the fine tuning of the slice gradient compensation.
`at`	Acquisition time.
`ni`	Loop count for 2D imaging and inner loop count for 3D imaging.
`ni2`	Not used in 2D imaging, but is used in array 2D imaging, and is the outer loop count for 3D imaging.
`phi`	Angular range (180° or 360°) in 2D and 3D imaging.
`theta`	Angular range (180° or 360°) in 3D imaging.
`trise`	Gradient settling time.
`te`	Spin echo time.
`tpe`	Duration of dephasing period of read gradient.
`tph`	Time for setting the pulse phase ($T_{1\rho}$ only).
`tr`	Recovery time.
`p1, tpwr1`	Duration and transmitter power of 90° pulse.
`pi, tpwri`	Duration and transmitter power of `sr`, `ir` pulse.
`pj, tpwrj`	Duration and transmitter power of spin lock pulse ($T_{1\rho}$ only).

`sat`	Delay between the first two saturation pulses in the `aps` sequence.
`nsat`	Number of pulses in the `aps` sequence.

The following parameters are string-type parameters related to the BP package:

`orient`	String of three letters assigning the orientation for the x-, y- and z-gradients. `orient='xyz'` assigns direction x to the x-gradient, direction y to the y-gradient, and direction z to the z-gradient. `orient='yzx'` gives a yz slice in a 2D imaging sequence. For 3D sequences, the sequence of gradients must comply with a clockwise-oriented coordinate system.
`p1pat`	Pulse pattern 90° pulse. The pattern selected is modified by `bptype`.
`pwpat`	Pulse pattern 180° pulse. The pattern selected is modified by `bptype`.
`bptype`	Sets slice-selective excitation. Two strings are valid: `bptype='noslice'` results in a non-slice-selective excitation, and `bptype='slice'` results in a slice-selective excitation.
`prep`	Sets weighting and can take the following values: `prep='none'` for no NMR weighting in the preparation phase, `prep='sr'` for T_1 weighting using saturation recovery, `prep='ir'` for T_1 weighting using inversion recovery, `prep='aps'` for T_1 weighting with aperiodic saturation, and `prep='t1r'` for $T_{1\rho}$ weighting.

10.5 Artifacts in BP Imaging

This section is intended to assist you in identifying problems while you carry out BP imaging sequences. Particular problems and their effects imposed on the resulting images are described.

Object Size and Field of View

BP imaging is based on profiles and can reconstruct planes with circular boundaries or volumes with spheres as boundaries. Probes used for BP imaging must fit in these boundaries for obtaining proper images. Therefore, make sure to meet these conditions:

- Take the maximum diameter of your probe and increase the diameter by 20% to set the field of view in your imaging setup.
- Align the probe's geometric center with the center of the field of view. Make sure that the probe under investigation fits into the given boundaries.

If the probe exceeds the given boundaries, the profile will suffer from folding (aliasing) artifacts and exhibit nonzero values on the left and right edges as depicted in Figure 126. In the reconstruction process, these effects are interpreted like a step function with unlimited slope. The reconstruction itself uses the derivative and therefore its result will be imposed.

To prevent distortion, increase the field of view, readjust the probe alignment with regard to the center of the field of view, or take both actions.

Dynamic Range Limitations

In a simple approach, BP image reconstruction can be viewed as adding each profile onto the slice or volume, taking its particular orientation (angle `phi` and `theta`) into account. (In reality, a filter or convolution process is involved, together with a linear interpolation). Therefore, the center points of all profiles are added to the center point of the slice or volume. On the other hand, the center point of a profile corresponds to the dc offset of the

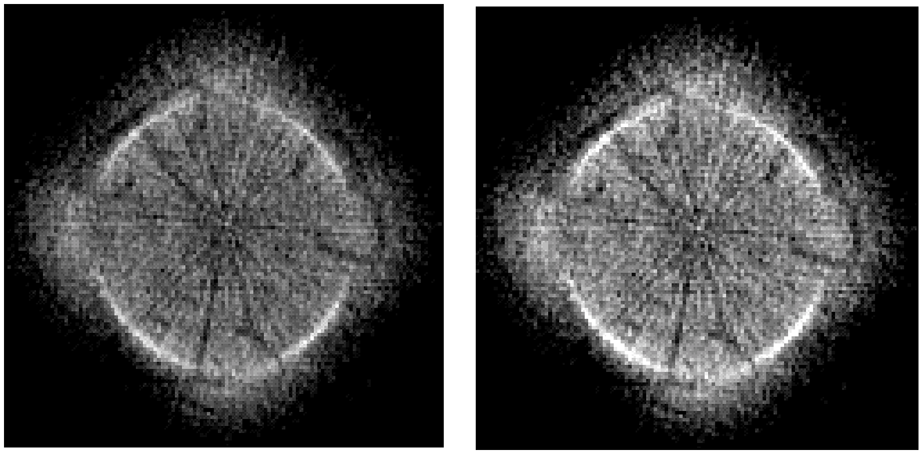


Figure 126. Distorted Images

acquired magnetic resonance signal. Any imperfections in dc offset correction result in a small additional intensity in the center of the profile.

These imperfections are added up in the reconstruction process and can cause a significant, larger central spike in the middle of the slice or volume, which degrades the dynamic range of the whole slice or volume. As a result, you'll see a white dot, or in case of a weighted FT, a bright area in the center of the slice or volume.

Image Degradation from a Single Projection

In BP imaging, one faulty projection can spoil the reconstructed slice or volume. There can be two reasons for a faulty projection:

- Saturation during the start of imaging sequence. If the recovery time, `tr`, is too short and no dummy scans are used prior to acquisition, a strong saturation takes place in the first projection. This saturation results in high signal amplitude for the first projection compared to the following projections.
- Distortions for a projection caused by radiation from outside (e.g., second spectrometer nearby) or by arcing in the probe (e.g., too much transmitter power).

Figure 127 shows the effect of saturation during the start of an imaging sequence on a 2D BP image. The first projection dominates the complete image and its pattern is superimposed on it. For comparison, the correct image is shown on the right side. To solve this problem, use dummy scans to achieve steady state before acquisition and/or to increase the time, `tr`.

Circular Image Intensity Modulation

BP imaging of semirigid or solid materials requires a short `te`, thus moving the spin echo from the center of the signal to the left side and reducing `dy` to a minimal value. In this case, the acquisition starts directly after the refocusing rf pulse. Because of this time constraint, the signal typically shows a small FID on the left side, which results from the imperfections of the pulse. In the Fourier transform, this FID (originating from the leftmost part of the signal) is transformed to a high frequency modulation of the profile. Since the FID is similar for all projection angles, the modulation is similar as well. After reconstruction, a

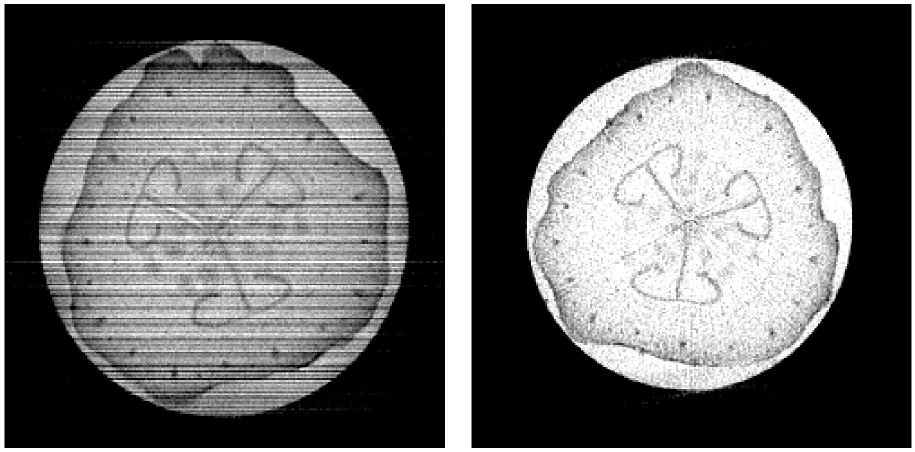


Figure 127. Saturation in First Projection

circular or spherical modulation is obvious in the slice or volume. Figure 128 shows an example.

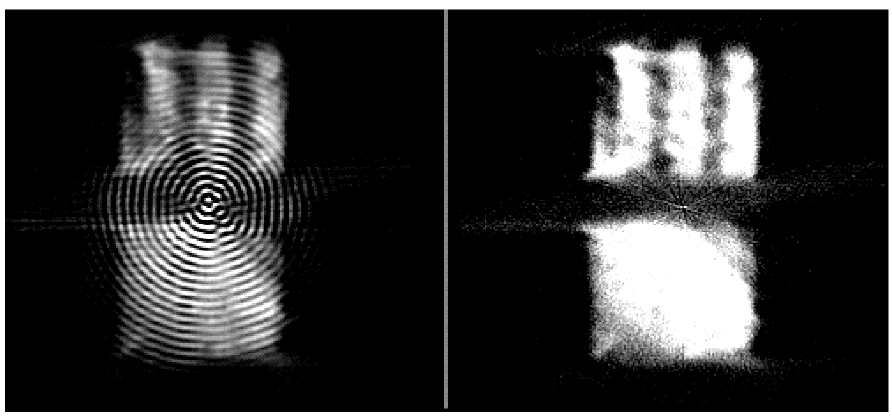


Figure 128. Circular or Spherical Modulation

To solve the problem, perform the following corrective actions.

- Increase the spin echo time, `te`, and move the spin echo to later time regimes (to the right). The loss in signal to noise must be compensated by a longer measurement time.
- If a new acquisition of the data is not possible, use a weighted FT, which reduces the effect of the residual FID.

Image Intensity Modulation

The image intensity gets modulated (as shown by the example in Figure 129) if several projections are faulty.

The following conditions might cause modulation:

- Gradient switch-off during acquisition because of an overrange situation detected during the acquisition in the microimaging cabinet.
- Arching in the probe during the acquisition.

Figure 129. Image Intensity Modulation

- Incomplete coverage of the angle for phi or theta set by the user.

To solve this problem, redo the acquisition and remedy the reason for the faulty or missing projections.

Image Reconstruction Using Off-resonance Spin Echoes

BP imaging requires an "on-resonance" condition to align all profiles in one central point. If profiles are acquired in "off-resonance" condition, the information in the profiles is shifted on the profiles' axis according to the gradient. This misalignment results after reconstruction in an image like the one shown in Figure 130. It is obvious that the contributions of each profile to a particular pixel position were smeared on a half circle.

The only solution for this problem is to redo the scan and adjust a proper on-resonance condition.

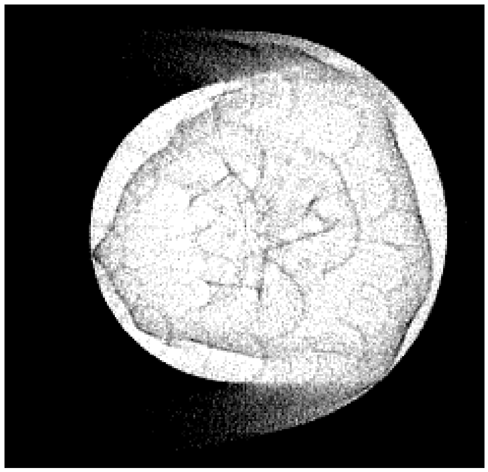


Figure 130. Misaligned Profiles

Profile Degradation Induced by Gradient Switching

Theoretically, the two projections from 0° and from 180° of the same object should be the same except that one is the mirror image of the other. Figure 131 shows a projection from 0° on the left side and a projection of 180° on the right side. Mirroring the projection of the right side and superimposing them results in Figure 131. Notice that both projections originate from the same object, but they show variations in the amplitudes. Since this problem is independent from gradient settling times, it can only be related to a shift of the B_0 field. This shift is caused by gradient switching and has a long time constant.

Experience has shown that the resulting images can be improved by not only taking a 180° angular view but a full 360° view (which includes doubling the number of projections). However, this problem needs further investigation.

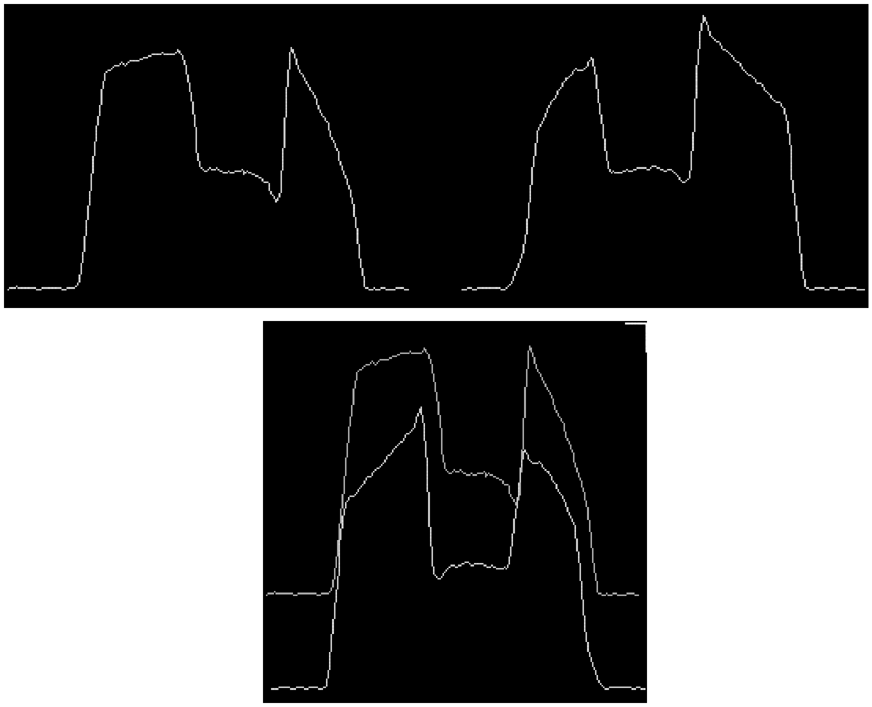


Figure 131. B_0 Field Shift

Sample Probe Preparation

To obtain the first BP image, you might want to use a phantom setup such as the one shown in Figure 132.

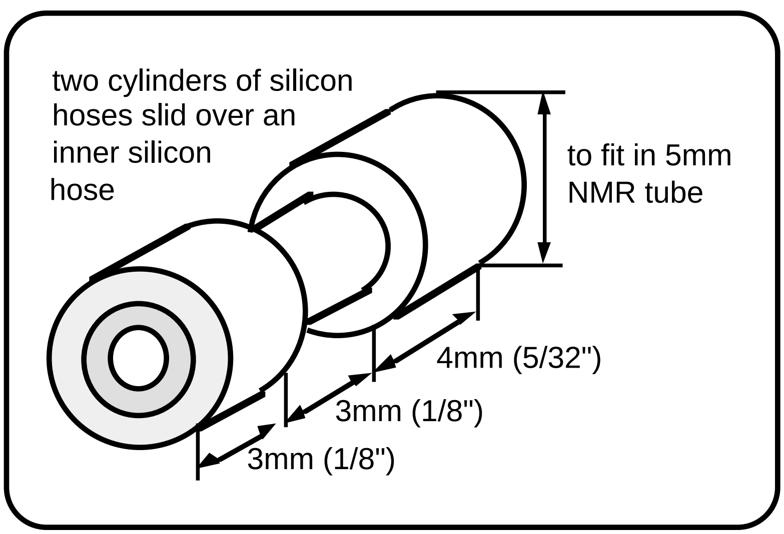


Figure 132. Phantom Setup for BP Imaging

The phantom is based on two silicone hoses with different diameters constructed as follows:

1. From the hose with the smaller diameter, cut one piece, 10 mm (13/32 inches) long.
2. From the hose with the larger diameter, cut two pieces, 3 mm (1/8 inches) and 4 mm (5/32 inches) long.
3. Slide the larger diameter pieces onto the smaller diameter piece, as shown in Figure 132. Friction should hold the pieces in place.
4. Put the phantom in a cylinder of an NMR tube. The cylinder should have a 5 mm diameter and be about 20 mm (3/4 inches) long.
5. Insert this setup in the solenoid coil of the microimaging probe.
6. Insert the probe into the bore of the magnet.

10.6 BP Macros and Programs Details

This section describes in more detail the reconstruction macro and programs.

Macro bp_reco

The BP package contains the macro bp_reco to control the reconstruction process. This macro initializes and executes the reconstruction of a 2D, 2D arrayed, or 3D data set. The parameter ni2 is used to decide between the 2D (ni2 or nv2<=1) or the 3D (ni2 or nv2>1) case. The following intermediate files are generated during reconstruction to pass information from one program to the other:

mchelp	Executable command file to apply the magnitude calculation.
bp_cmd	Parameter file to control the bp_2d and bp_3d programs.
bphelp	Executable command file to run the bp_2d and bp_3d programs.

bp_reco first removes these intermediate files and already reconstructed slices. Because the VNMR software does not allow a magnitude calculation on the profiles obtained after a Fourier transform, a stand-alone program, bp_mc, serves this purpose and is executed using mchelp. The next step puts parameters to the file bp_cmd that controls the operation of the programs bp_2d and bp_3d. The individual parameters are explained in conjunction with these programs. Again, a file bphelp serves to execute the bp_2d and bp_3d programs. After reconstruction, one or more FDF files exist in the experiment datdir directory.

Programs bp_mc, bp_sort, bp_2d, bp_3d

The BP package contains the programs bp_mc, bp_sort, bp_2d, and bp_3d.

bp_mc	Performs a magnitude calculation. Used prior to bp_2d and bp_3d.
bp_sort	Shuffles projections obtained using an arrayed parameter in a 2D acquisition in the order required by the bp_2d program.

`bp_2d`, `bp_3d` — Controlled by a command file that holds several lines. Each line contains the parameter name in the first position and the value of the parameter to be used in the second position, separated by a blank or a tab. Adding a comment to a line (or a particular parameter setting) is possible by using a blank or tab as a separator. The value of the parameter may not be assigned by an equals symbol (=). The command file holds two classes of parameters, labeled essential and optional. The essential parameters have to be specified in the command file, whereas the optional parameters are derived from the essential parameters and some general assumptions if they are omitted

Table 22 provides a summary about the valid parameters and their defaults.

Table 22. Parameters Passed to the `bp_2d` and `bp_3d` Programs

Parameter Keyword	*Parameter Type*	*Essential*	*Optional*	*Default Setting*
`prof_file`	string	x		
`m_size`	int	x		VNMR `np`
`i_size`	int	x		VNMR `np`
`n_phi`	int	x		
`n_theta`	int	x		
`in_memory_prof`	int		x	0
`filter_name`	string		x	`band_pass`
`filter_bw`	double		x	1.0
`meta_image`	string		x	`prof_file` + ".meta"
`prof_filt1`	string		x	`prof_file` + "filt1"
`prof_filt2`	string		x	`prof_file` + "filt2"
`image_file`	string		x	`prof_file`
`r_size`	int			`x m_size`
`m_center_x`	double		x	`m_size/2.0`
`m_center_y`	double		x	`m_size/2.0`
`m_center_z`	double		x	`m_size/2.0`
`r_center_x`	double		x	`m_size/2.0`
`r_center_y`	double		x	`m_size/2.0`
`r_center_z`	double		x	`m_size/2.0`
`theta_start`	double		x	0.0
`theta_end`	double		x	`theta_start` + 180.0
`phi_start`	double		x	0.0
`phi_end`	double		x	`phi_start` + 180.0

Parameters Set by bp_setup

The following parameters are set by the macro `bp_setup`. Refer to page 234 for a detailed description of this interface.

`prof_file` — Name of the profile file (e.g., `bp3d_prof`). Do not omit.

`m_size` — Specifies the measurement size and is equivalent to the number of complex data points during acquisition or to the number of real valued data points in the profile file. If `m_size` is not set, `bp_3d` tries to obtain its value from the profile file and sets `m_size=np/2`.

i_size	Size of the reconstructed volume. The resulting i_size images are i_size*i_size large. Specifying i_size > m_size results in an enlargement or in a reduction (i_size < m_size) in the number of pixels used. This feature allows achieving a reconstruction for a fast inspection of large data set using reduction. If i_size is not set, bp_3d tries to obtain its value from the profile file and sets i_size=m_size= np/2.
n_phi	Number of projections used for the phi loop, usually the same as ni. n_phi has to be specified by the user and cannot be derived from the information given in the profile file. The phi loop is the inner loop during acquisition.
n_theta	Number of projections used for the theta loop, usually the same as ni2. n_theta has to be specified by the user and cannot be derived from the information given in the profile file. The theta loop is the outer loop during acquisition.
in_memory_prof	Controls the storage of profile data in memory in order to save overhead for disk I/O, thus accelerating the reconstruction process. Generally, in_memory_prof can be set to 1 if i_size<256. Otherwise, setting in_memory_prof=0 is recommended to avoid keeping too much data in memory and causing unnecessary swapping to the hard disk.
filter_name	Selects filter to be used in the reconstruction process. Four different filters are implemented: (1) band_pass is a purely magnitude-like filter, (2) si_low_pass is a magnitude filter modulated with a si = (sin x) / x function, (3) cos_low_pass is a cosine-modulated magnitude filter, and (4) hamming is a Hamming filter. Filters 2, 3, and 4 are used to suppress high spatial frequencies.
filter_bw	Specifies the bandwidth of the filter function. filter_bw is valid for 1.0 or less. For a value of 1.0, no additional spatial frequency cutoff is performed with regard to the filter function used. Smaller values lead to a cutoff and a smoothed image. For a Hamming filter, filter_bw=0.54 is recommended.
meta_image	Name of the intermediate file between the first and second cascade of the 3D BP. If meta_image is not specified, it is automatically set up.
prof_filt1 prof_filt2	Intermediate files within the first and second cascade, respectively.
image_file	Name mask for the resulting slices of the 3D volume. Each slice is indicated by an extension to image_file with iii=[000,001,002,...,i_size-2, i_size-1]. If image_file is not set, the default mask is prof_file. Any subsequent reconstruction overwrites the already reconstructed slices.
r_size	Provides partial reconstruction facilities to assist in off-resonance conditions. r_size must be greater than or equal to 0 and must be less than m_size to achieve full support on the unit ball given by m_size.
m_center_x m_center_y m_center_z	Measurement center definitions that allow compensation for different definitions used for the position of frequency = 0 in the profile (the center value). Typically, they are set to m_size/2.0.
r_center_x r_center_y r_center_z	Reconstruction center definitions used to compensate an offset in an off-resonance condition. In the case of no off-resonance condition, they are set to m_size/2.0.

`theta_start`
`theta_end`
`phi_start`
`phi_end`
	Specify the start and end values of the angles used for 3D BP acquisition. The angles are set using degrees instead of radians. The angle increment between subsequent steps of theta are derived by `theta_increment=(theta_end – theta_start)/n_theta` and can be positive or negative. The same applies to `phi`. Typically, the difference between the start and end values is 180°. This is the default case. If the difference between the start and end is 360°, both start and end have to be specified in the command file.

10.7 References

The following bibliography lists the references that were important contributions to the research and writing of this chapter.

Marr, R. B.; Chen, C. N.; Lauterbur, P. C. On Two Approaches to 3D Reconstruction in NMR Zeugmatography. In *Mathematical Aspects of Computed Tomography*, **8:**225-240, edited by G.T. Herman and F. Natterer, Springer-Verlag, New York, 1981.

Peters, T. M. Algorithms for Fast Back- and Re-Projection in Computed Tomography. *IEEE Trans. Nucl. Sci.* **1981**, *28***,** 4.

Rowland, S. W. Computer Implementation of Image Reconstruction Formulas. In *Image reconstruction from Projections. Implementation and Applications*, edited by G.T. Herman, Springer-Verlag, Berlin, Heidelberg, New York, pp 9ff, 1980.

Project Report "3D - Backprojection reconstruction," Fraunhofer Institute Biomedical Engineering (IBMT), St. Ingbert, 1992.

Chapter 11. Interactive Image Planning

11.1 Introduction

You can perform interactive image planning on an image. When you enter the command `iplan`, the interactive image planning program opens. The `iplan` macro also executes the transverse slice specification tool (`tbox`). By choosing a button in the `iplan` graphics area, you can stretch, tilt, and move the `tbox` tool. You can also adjust the number of slices and the area that they cover. Clicking the **Exit** button executes the `rsliceplan` macro to load these settings for the next images.

11.2 Starting the Planning Session

To start planning:

1. Open the scout image, preferably more to the right of the display area.
2. Enter the command `iplan`.

   A vertical column of boxes appears on the left side of the display area as shown in Figure 133.

   The cursor has also changed to a pointing hand. The boxes are active controls that you can select with the cursor and a left mouse click. Table 23 describes the controls.
3. Select **Position**.
4. Press and hold down the left mouse button and move the center of the current stack to the desired place on the image. Release the mouse button.

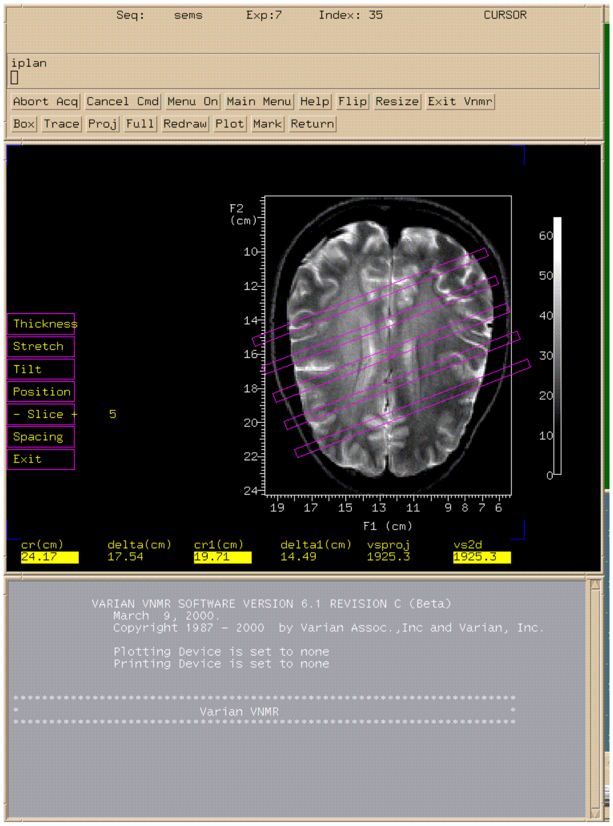


Figure 133. Interactive Image Planning Interface

5. Select **Tilt** and rotate the stack to the desired orientation with the left mouse button. Add slices to the stack by clicking near the + in the Slice box, or remove slices by clicking near the –.

Table 23. `iplan` Controls

Thickness	Adjust the slice thickness. The current value is displayed on the graphics area.
Stretch	Adjust the width of the set of slices. The width is the dimension orthogonal to the number of slices. Therefore, the size of a slice is defined by its width and thickness. The width is also the width of the field of view.
Tilt	Rotate the stack of slices about their center.
Position	Adjust the position of the center of the stack of slices.
– Slice +	Add or subtract a slice to the stack.
Spacing	Adjust the spacing between slices. Therefore, the number of slices, their thickness, and spacing determine the height of the field of view.
Exit	Exit the planning mode and show a list of experiments to be used as targets. The menu above the display region also reflects the possible targets. When you click one of these buttons, the planning parameters are transferred to the target experiment ready for use.

Other planning operations include setting the width of the slices, thickness of each slice, and interslice spacing.

6. When the stack of slices correctly overlays the scout image, click on **Exit**, select the target experiment from the list, and transfer the image prescription by clicking on the appropriate menu button.

   To exit from the planning process without making any changes to a target experiment, press **Return** on the keyboard.

Appendix A. Commands, Macros, and Parameters

Sections in this appendix:

This appendix summarizes commands, macros, and parameters necessary, or at least particularly useful, for imaging experiments. For a list of entries, refer to the table of contents at the front of this manual. In the section "Commands and Macros for Processing and Display," page 278, commands are identified by the code "(C)" at the end of header line and macros are identified by the code "(M)." All commands and macros are entered on the VNMR command line. The code letter "U" at the end of the header line (e.g., (U) or (M, U)), means the command can be entered on a UNIX command line. Note that the UNIX syntax is always different from VNMR syntax.

There is an important distinction between VNMR commands and macros:

- Commands are compiled, executable files incorporated into the VNMR software.
- Macros are interpreted text files written in Varian's MAGICAL language.

Macros therefore have one distinct advantage to the user: they can be modified and customized. See the manual *VNMR User Programming* for a complete description of macro language syntax and tools.

Most parameters found in VNMR (such as `np`, `d1`, or `sw`) are common to all experimental applications. For general information on parameters, parameter entry, and definitions, refer to the manuals *VNMR Command and Parameter Reference*, *VNMR User Programming*, and *VNMR Pulse Sequences*.

A.1 Setting the Path to Imaging Macros

Most of the macros described in this appendix are in a special directory for imaging macros, `/vnmr/maclib/maclib.imaging`. VNMR is directed to look in this directory through the `sysmaclibpath` parameter.

To set the parameter `sysmaclibpath`:

- Set it directly, for example, by entering it through the VNMR command line:
  `sysmaclibpath='/vnmr/maclib/maclib.imaging'`
- Set it by using the VNMR menus system:

a. Click on the Main menu button, then Setup, and finally App Mode.

b. Click on the Imaging button to set `sysmaclibpath` to the `maclib.imaging` directory.

This approach is recommended because it also creates `sysmaclibpath` if it does not already exist. This procedure can also be used to set `sysmenulibpath` and `syshelppath`.

A.2 Macros for Setting Up Experiments

Many macros are available for setting up NMR experiments. This section summarizes the most useful macros for imaging experiments.

`creategtable` **Create gradient calibration file**

Syntax: `creategtable(file)`

Description: Generates a new gradient calibration file for gradient sets with nonisotropic strengths. Gradient calibration constants, such as `gmax` (maximum gradient strength) and `trise` (rise time of a gradient from 0 to `gmax`) are stored in the directory `/vnmr/imaging/gradtables`. Each gradient set installed with the system should have a corresponding file in this directory describing its gradient strength and rise time. These `gradtables` text files can be manually copied and edited to add or modify gradient calibrations.

`creategtable` is supplied as a convenient method of generating a new file through a series of prompted responses. It should be used to make `gradtables` entries for gradient sets that have isotropic strengths (i.e., strength on X, Y, and Z axes) and nonisotropic gradient strengths.

Arguments: `file` is the new gradient calibration file name.

Examples: `creategtable('asg33')`

Related:

`createpfgtable`	Create gradient calibration file (nonisotropic strengths) (M)
`gmax`	Maximum gradient strength (P)
`trise`	Gradient rise time (P)

`createpfgtable` **Create new gradient calibration file (nonisotropic strengths)**

Syntax: `createpfgtable(file)`

Description: Generates a new gradient calibration file for gradient sets with nonisotropic strengths. Files are created in the `/vnmr/imaging/gradtables` directory in cases where the X, Y, and Z axes have different maximum gradient strengths.

Arguments: `file` is the new gradient calibration file name.

Examples: `createpfgtable('pfg5mm')`

Related:

`creategtable`	Create gradient calibration file (isotropic strengths) (M)
`gxmax,gymax,gzmax`	Maximum gradient strength for each axis (P)
`trise`	Gradient rise time (P)

`deccgo` **Perform an action for decctool (M)**

Syntax: `deccgo`

Applicability: Systems with digital eddy current compensation (DECC).

Description: Executed by the decctool program when the **Save & Go** button is pressed. By default, `deccgo` executes `go`, but `deccgo` macros that perform other actions can be created. If the `deccgo` parameter exists, this macro executes the contents of the parameter.

Related: `deccgo` Action to perform for decctool (P)

`deccgo` Action to perform for decctool (P)

Syntax: `deccgo`

Applicability: Systems with digital eddy current compensation (DECC).

Description: Contains a command that is executed by the `deccgo` macro. By default, the `deccgo` parameter does not exist, and the `deccgo` macro, by default, executes a `go` command. If the parameter is created in an experiment with the command `string('deccgo')`, whatever string value the parameter contains is executed as a command by the `deccgo` macro instead of `go`.

Examples: `deccgo='ga'`

Related:
`deccgo` Perform an action for decctool (P)
`decctool` Open decctool window (M,U)
`string` Create a string variable (C)

`decctool` Open decctool window (M,U)

Syntax: `decctool`

Applicability: Systems with digital eddy current compensation (DECC).

Description: Starts the decctool program to adjust eddy current compensation parameters and sets gradient gain, slew rate, and duty cycle.

`exparray` Array a numeric parameter

Syntax: `exparray<(parameter,start,end,number)>`

Description: Arrays any numeric parameter in exponentially increasing steps. `exparray` provides a convenient method of arraying a numeric parameter when an exponentially changing increment between arrayed values is desired, such as in T_1 or T_2 experiments. It works with any arrayable parameter and generates arrayed values in ascending or descending order.

When other parameters are already arrayed, the parameter `array` is updated. If more advanced array capabilities (such a simultaneous arrays) were specified through `array`, the value of a parameter might need to be corrected after use of `exparray`.

Arguments: `parameter` is the name of parameter to be arrayed. The default is an interactive mode in which you are prompted for the parameter. Only numeric parameters can be arrayed.

`start` is the value of the first array element.

`end` is the value of the last array element.

`number` is the total number of array values.

Examples:
```
exparray
exparray('d2',0.01,2,10)
```

Related: `array` Easy entry of linearly spaced array values (M)

`array`	Parameter order and precedence (P)
`setarray`	Set up a parameter array (M)

`flash3d` **Retrieve parameters for FLASH3D imaging experiment**

Syntax: `flash3d`

Description: Retrieves the standard parameters for the FLASH3D imaging experiment from `/vnmr/parlib`.

`gems` **Load default parameters from gems.par**

Syntax: `gems`

Description: Loads the default parameters from the `gems.par` file into the current experiment. `gems` first searches for a parameter file in `$HOME/vnmrsys/parlib` and loads the file if it is present; otherwise, the file is loaded from the `/vnmr/parlib` directory.

Examples:
```
gems('/$HOME/vnmrsys/parlib/gems.par/H1')
gems('/vnmr/parlib/H1')
```

`imprep` **Set up rf pulses, imaging and pulse power levels**

Syntax: `imprep`

Description: A one-pass macro that sets all gradient and pulse power levels in imaging and localized spectroscopy experiments. All applications that use list parameters (`plist`, `patlist`, `pwrlist`, etc.) can be set up with `imprep`.

`imprep` sets all of the following parameters, where applicable:

- Power levels for all pulses found in `plist`
- Readout gradient strength (together with `sw`)
- Up to three phase encode gradient levels
- Slice and/or voxel selection gradient levels

`imprep` requires that the `rfcoil` parameter be set to the name of a valid entry in the `pulsecal` database file, previously created with the `pulsecal` macro. The information found in `pulsecal` is used to compute the pulse power levels for each rf pulse required to give the flip angles found in `fliplist`.

`imprep` uses the names found in `pwrlist` to determine which power level corresponds to which rf pulse. The rf pattern parameter names found in `patlist` are used by `imprep` to obtain the names of the pulse shapes that correspond to each rf pulse in the sequence. The pulse integral (relative to a square pulse) found in the header of each rf shape file is used with the pulse calibration found in `pulsecal` to calculate the value for each power level.

The readout gradient, `gro`, is determined with an algorithm that attempts to balance possible chemical shift errors from too low a gradient strength against excessive bandwidth (spectral width, `sw`), which can result in reduced signal-to-noise. Once a value for the readout gradient is selected, spectral width is determined through the relationship `sw`=γ*`lro`*`gro`. If the values of `gro` or `sw` selected by `imprep` are unsatisfactory for any reason, use the macro `setgro` to explicitly set `gro`.

`imprep` computes and sets the phase encode increment and timing, and the indirect dimension “spectral width” associated with each phase encode

dimension present. The gradient*time integral for the increment between phase encode levels is governed by the requirement that the spins at the edges of the field-of-view undergo a phase shift of 180°. The phase encode time, tpe, is set to 2*trise, and the phase encode increment is then computed, in G/cm, to satisfy the expression γ*tpe*lpe*gpe=1. Some imaging sequences might internally alter the value of tpe, with a corresponding change in gpe, where timing of the sequence events allows. imprep performs these computations for each phase encode gradient found in the sequence. A 2D sequence generally has one readout dimension and one phase-encode dimension, described by the parameters gpe, sw1, and tpe. A second or third phase encode dimension is described by the triad of parameters gpe2, sw2, tpe2, and sw3, gpe3, and tpe3, respectively. The spectral width associated with each phase encode dimension is computed as 1/tpe (or 1/tpe2, etc.), and has no physical significance. sw1 is present to provide compatibility with analytical 2D NMR data processing and display routines in VNMR.

Slice and voxel selection gradients are computed by imprep based on the pulse lengths and shapes of all relevant pulses in the sequence. imprep uses the gradient names found in sslist to determine which spatially selective gradients correspond to each rf pulse. Together with the bandwidth for each pulse, found in the header of each shape file, imprep computes the slice or voxel selection gradient to achieve the appropriate slice thickness or voxel dimension. imprep assumes that the slice thickness for imaging experiments is specified by the parameter thk, and that voxel dimensions for voxel experiments are specified by the three parameters vox1, vox2, and vox3. Gradient levels are then calculated from the relationship gss=BW/(γ*thk) for slice selection, or gvox1=BW/(γ*vox1) for voxel selection. Where there are two or more pulses used with the same slice select gradient, gss is determined by the rf pulse with the narrowest excitation bandwidth.

Related:	fliplist	Flip angle list (P)
	gro	Readout gradient strength (P)
	gvox1,gvox2,gvox3	Gradient strength for voxel selection (P)
	plist	Pulse length parameter list (P)
	patlist	Pulse shape parameter list (P)
	pwrlist	Pulse power level parameter list (P)
	pulsecal	Create, modify, delete entry in pulsecal rf calib. file (M)
	rfcoil	RF pulse calibration identity (P)
	setgpe	Set phase encode gradient levels (M)
	setgro	Set readout gradient strength and spectral width (M)
	setgss	Select slice or voxel selection gradient levels (M)
	setvgrad	Set voxel-selection gradient strengths (M)
	sslist	Gradient parameter names list (P)
	sw	Spectral width in directly directed dimension (P)
	sw1	Spectral width in first indirectly detected dimension (P)
	sw2	Spectral width in second indirectly detected dimension (P)
	sw3	Spectral width in third indirectly detected dimension (P)
	tpe	Duration of the phase encoding gradient pulse (P)
	tpe2,tpe3	Length of 2nd and 3rd phase encoding gradient periods (P)
	thk	2D imaging plane slice thickness (P)

isis **Retrieve parlib parameters for ISIS imaging experiment**

Syntax: isis

Description: Retrieves the standard parameters for the ISIS imaging experiment from `/vnmr/parlib`.

ldof **Load resonance offset frequency**

Syntax: `ldof`

Description: Initializes the resonance transmitter offset frequency, `resto`, to the value saved in `$HOME/vnmrysy/H1offset`.

Examples: `ldof`

Related:

`resto`	NMR resonance offset frequency (P)
`setof`	Measure and save resonance transmitter offset frequency

mems **Retrieve parlib parameters for MEMS imaging experiment**

Syntax: `mems`

Description: Retrieves the standard parameters for the MEMS imaging experiment from `/vnmr/parlib`.

movetof **Move transmitter offset**

Syntax: `movetof <(frequency)>`

Description: Moves the transmitter offset parameter `tof` so that the current cursor position, defined by `cr`, becomes the center of the spectrum. If referencing was used, `movetof` maintains the referencing.

Arguments: `frequency` specifies the transmitter frequency rather than using the cursor position to define the frequency. This provides a convenient method of moving the transmitter frequency outside the current spectral window.

Related:

`cr`	Cursor position in directly detected dimension (P)
`minsw`	Reduce spectral width to minimum required (M)
`movesw`	Move spectral window according to cursors (M)
`tof`	Frequency offset for observe transmitter (P)

movepro **Move imaging readout position**

Syntax: `movepro`

Description: Sets the readout position for an image or image projection to a point defined by the position of the cursor (the `cr` parameter).

`movepro` works with either a 1D display (a projection or trace along F2) or 2D display, in either single cursor or box modes (only the position of the cursor in the F2 readout dimension is used; the position of the cursor in the F1 phase-encode dimension does not matter).

`movepro` determines the position of the cursor relative to the gradient origin and sets the parameter `pro` to this value, independent of image orientation. Because `pro` is measured in dimensional units (like mm or cm), and cursor position is stored internally (in hertz), `movepro` works in Hz, taking into account any spectral referencing that might have been set, and converts to cm or mm to assign the value of `pro`.

To use `movepro`: (1) Display an image, image projection or trace, (2) Move the cursor to the position along the readout axis you desire to be at the center of the next image acquisition, and (3) Enter `movepro`.

`movepro` has no effect on the value of `tof` (which is normally not used to define any positional information in imaging). Unlike `movetof`, the image or projection display is unchanged, and no redisplay in “full” mode should be necessary.

To accurately center an image or projection, move the box cursors to the edges of the imaged object, use the macro `split` to place the cursor at the exact midpoint of the box, then type movepro.

Related:

`lro`	Field of view size for readout axis (P)
`movetof`	Move transmitter offset (M)
`pro`	Position of image center on the readout axis (P)
`resto`	NMR resonance offset frequency (P)
`split`	Split difference between two cursors (M)

`mvfov` Move the field-of-view from one experiment to another

Syntax: `mvfov(<from_exp>,to_exp)`

Description: Copies the field-of-view parameters, which describe the imaging orientation and position in the current experiment, to another experiment.

The destination experiment can be any type of imaging application, as long as it uses the same set of field-of-view parameters. For example, the imaging position and orientation used to acquire a SEMS image can be copied with `mvfov` to a second experiment set up to acquire a FLASH image.

The following parameters are copied by `mvfov`:

lpe	`phi`	`psi`	`resto`	`theta`
`lro`	`pro`	`pss`	`rfcoil`	`thk`

If `mvfov` is used with only one argument, the field-of-view parameters are automatically copied from the current experiment.

Arguments: `from_exp` is the number of the current experiment from which FOV parameters are copied. The default is current experiment.

`to_exp` is the number of the destination experiment in which the copied FOV parameters are placed.

Examples:
```
mvfov(2,5)
mvfov(4)
```

Related:

`mf`	Move FIDs between experiments (C)
`mp`	Move parameters between experiments (C)
`transfer`	Move parameters to target experiment (M)

`offset` Calculate and display absolute frequency offset at cursor

Syntax: `offset<('silent')><:parameter>`

Description: Determines the absolute frequency offset at the spectral position defined by the cursor (parameter `cr`) and accounts for any spectral referencing that might have been set. `offset` finds the frequency at a particular spectral position relative to the base spectrometer frequency `sfrq`. It displays the result of its calculation, and returns the value, which can optionally be assigned to a parameter or internal macro variable.

Use offset in a 1D proton spectrum to determine the proper spectral reference frequency to be assigned to `resto` in imaging experiments. It can also be used

to determine spectral frequencies for presaturation, fat suppression, chemical shift selective imaging, etc.

The displayed value of `sfrq` is the sum of the base spectrometer frequency (specified by the parameter `tn`) and the value of `tof`. Thus, if a point at the center of the spectrum is used, `offset` returns a value equal to `tof`, and not zero.

CAUTION: **Because most imaging spectrometers either do not have lock hardware, or run imaging in unlocked mode, the solvent parameter should be set to 'none' in both the imaging experiment and any 1D spectral experiment used to determine frequency offsets. Having solvent = 'CDCl3', for example, results in improper frequency assignments in any imaging experiment with solvent = 'none'.This can result in errors in slice and readout position, or failure of frequency dependent functions, such as water suppression.**

Arguments: `'silent'` is a keyword to not display the frequency offset value. The default is to display the value.

`parameter` is a variable (such as the parameter `tof` in the example below) that, if present, is loaded with the calculated offset frequency value.

Examples: `offset`
`offset:satfrq`

Related:

`cr`	Cursor position in directly detected dimension (P)
`resto`	NMR resonance offset frequency (P)
`sfrq`	Transmitter frequency of observe nucleus (P)
`solvent`	Lock solvent (P)
`tof`	Frequency offset for observe transmitter (P)

`pulsecal` **Create, modify, or delete entry in pulsecal rf calibration file**

Syntax: (1) `pulsecal<(name,pattern,length,flip,power)>`

(2) `pulsecal(name,'remove')`

Description: Adds new entries into an rf pulse calibration database file. This database file has the same name as the macro. `pulsecal` is used for automated setup of rf pulse powers in imaging and localized spectroscopy experiments.

The desired entry in the `pulsecal` file is selected with `rfcoil`, and provides the automated setup routines with information about the 90° pulse power performance. This information is used to compute the power levels required by all pulses found in `plist`. Each user has a private `pulsecal` file, found in the `vnmrsys` directory. If a `pulsecal` file does not already exist, `pulsecal` creates it when the first entry is made.

Some form of pulse length or power calibration data is required to provide the information necessary to create a new entry in `pulsecal`. This could be a simple 90° pulse length array using `s2pul`, an array of pulse power levels, or a more advanced calibration using an imaging or localized spectroscopy experiment (`tpwrcal`, for example).

Once an entry is made, it is used to determine pulse powers for a wide range of pulse lengths and shapes in all imaging and localized spectroscopy experiments. As long as the computed power levels remain within the linear performance range of the system (typically below `tpwr` of about 60) these power levels should be as accurate as could be determined through individual optimization.

Calibration entries in the `pulsecal` file are stored for a square pulse of the specified length. If a shaped pulse is used to determine the pulse calibration, `pulsecal` uses the integral of the shape to determine the corresponding power for a square pulse of the same length (which is why there is no pulse shape field in the `pulsecal` database file). This does not mean that nonsquare shaped pulses cannot be used to create new calibration entries, only that this information is converted and stored in the `pulsecal` file as if it were acquired with a square pulse. Thus, an entry created with a square pulse has the power level that was used as the argument to `pulsecal`. An entry created with a sinc pulse, however, has a much lower power level in the `pulsecal` file because the integral of a sinc pulse is only 17% of that of a square pulse. The pulse length is also adjusted to account for any round-off to the nearest integer pulse power level.

Arguments: `name` is the name of the rf coil or calibration.

`pulse_shape` specifies the rf pulse shape used to acquire the calibration data.

`length` is the length of the rf pulse (in μsec) used for calibration.

`flip` is the flip angle calibrated, in degrees.

`power` is the calibrated power level, in attenuator units.

If entered without arguments, `pulsecal` displays the current contents of the database file. Using `pulsecal` with syntax 1 creates an entry in the file `userdir+'/pulsecal'`. Using syntax 2 removes the entire line associated with the calibration name.

Examples:

```
pulsecal
pulsecal('quad6','sinc',2000,180,40)
pulsecal('quad8','remove')
```

Related:

	`imprep`	Set up rf pulses, imaging and pulse power levels (M)
	`plist`	Pulse length parameter list (P)
	`rfcoil`	RF pulse calibration identity (P)

`rescal` Calculate spatial resolution of an image

Syntax: `rescal<('silent')>`

Description: Computes and displays the 2D imaging pixel dimensions, in mm, for both the original data as acquired and the processed data as displayed on the screen.

Pixel size for the acquired data is computed as the field of view in the readout and phase-encode directions divided by the number of points (`np/2`) and the number of phase-encode increments (`nv`), respectively. Pixel resolution for an image as displayed on the screen might be different than for the raw image data because of zero filling. The displayed resolution is computed as the field of view in the readout and phase-encode directions divided by the Fourier transform sizes, `fn/2` and `fn1/2`, respectively. `rescal` returns these four values for optional use in a calling macro, and also displays the results in the VNMR text window.

Arguments: `silent` is a keyword to prevent display in the text window.

Related:

	`fn`	Fourier number in directly detected dimension (P)
	`fn1`	Fourier number in 1st indirectly detected dimension (P)
	`lpe`	Field of view size for phase encode axis (P)
	`lro`	Field of view size for readout axis (P)
	`np`	Number of data points (P)
	`nv`	Number of phase encode steps for 1st indirectly detected dimension (P)

rt **Retrieve FIDs**

Syntax: `rt<(file<,'nolog'>)>`

Description: Retrieves FIDs from a file into the current experiment.

Arguments: `file` is the name of the file that, with the suffix `.fid` added, contains the FIDs to be retrieved. The default is that the system prompts for the name (in that case, the name can be given without single quotes). If `file.fid` does not exist and `file.par` does, `rt` retrieves the parameters from `file.par`.

`'nolog'` is a keyword specifying that the log file is not to be retrieved.

Examples: `rt`
`rt('/vnmr/fidlib/fid1d')`

Related:

`fixpar`	Correct parameter characteristics in experiment (M)
`rtp`	Retrieve parameters (M)
`rtv`	Retrieve individual parameters (C)
`svf`	Save FIDs in current experiment (M)

rtp **Retrieve parameters**

Syntax: `rtp<(file)>`

Description: Retrieves parameters from a file into the current experiment.

Arguments: `file` is the name of the file that, with the suffix `.par` added, contains the parameters to be retrieved;. The default is that the system prompts for the name (in that case, the name can be given without single quotes). If `file.par` does not exist and `file.fid` does, `rtp` retrieves the parameters only from `file.fid`.

Examples: `rtp`
`rtp('/vnmr/stdpar/P31')`

Related:

`fixpar`	Correct parameter characteristics in experiment (M)
`rt`	Retrieve FIDs (M)
`rtv`	Retrieve individual parameters (C)
`svp`	Save parameters from current experiment (M)

s2pul **Set up parameters for standard two-pulse sequence**

Syntax: `s2pul`

Description: Converts the current experiment to an experiment suitable for the standard two-pulse sequence (S2PUL).

Alternate: S2PUL button in the 1D Pulse Sequence Setup Menu.

Related:

`spuls`	Load default single pulse sequence imaging parameters (M)

sediff **Retrieve parlib parameters for SEDIFF imaging experiment**

Syntax: `sediff`

Description: Retrieves the standard parameters for the SEDIFF imaging experiment from `/vnmr/parlib`.

sems **Retrieve parlib parameters for SEMS imaging experiment**

Syntax: `sems`

Description: Retrieves the standard parameters for the SEMS imaging experiment from `/vnmr/parlib`.

`setarray` Array any numeric parameter in constant-increment steps

Syntax: `setarray<(parameter,start,increment,number)>`

Description: Arrays a numeric parameter when a constant increment between arrayed values is desired. `setarray` works with any arrayable parameter and generates arrayed values in ascending or descending order.

When other parameters are already arrayed, `array` is updated. If more advanced array capabilities (such a simultaneous arrays) have been specified through `array`, its value might need to be corrected after use of `setarray`.

To repeat an experiment several times using the same parameter values (e.g., to perform a stability test), use `setarray` to array any parameter with an increment of 0.

Arguments: If no arguments are entered, the macro prompts for argument values.

`parameter` is the name of parameter to be arrayed.

`start` is the value of the first array element.

`increment` is the increment between successive arrayed elements.

`number` is the total number of array values.

Examples: `setarray`
`setarray('pw',10,10,4)` sets `pw=10,20,30,40`
`setarray('tof',-1000,500,4)` sets `tof=-1000,500,0,500`
`setarray('nt',1,0,10)` sets `nt=1,1,1,1,1,1,1,1,1,1`

Related:

`array`	Parameter order and precedence (P)
`exparray`	Array a numeric parameter (M)

`setflip` Set rf power levels to desired flip angle

Syntax: `setflip<(parameter,pattern,power,flip_angle)>`

Description: Computes the power level required to achieve a specified flip angle for any rf pulse. A valid entry in the `pulsecal` calibration file, specified through `rfcoil` is also required. `setflip` uses the pulse calibration, together with the integral of the pulse shape found in the header of the shape file, to compute the power level necessary to obtain the required flip angle.

Arguments: If no arguments are entered, the macro prompts for argument values.

`parameter` is the pulse length parameter.

`pattern` is the parameter holding the name of the pulse shape.

`power` is the power level parameter corresponding to the pulse.

`flip_angle` is the flip angle, in degrees.

Examples: `setflip('p2','p2pat','tpwr2',180)`

Related:

`imprep`	Set up rf pulses, imaging and pulse power levels (M)
`rfcoil`	RF pulse calibration identity (P)

`setgcal` Set the gradient calibration constant

Syntax: `setgcal`

Description: Determines the gradient calibration constant gcal by using a proton phantom of known dimensions. setgcal requests the linear dimension of the phantom in the readout direction. It uses the value entered, together with cursor separation of this dimension from the image profile and the strength of the readout gradient gro, or gzlvl1 if pulsed field gradients, to calculate gcal in units of gauss/cm-DAC units. You are then prompted whether this value should be entered. If you answer yes, it is stored as a system constant in the your global file.

Note that a particular value of gcal is closely related to the current eddy current compensation settings. If these settings are changed (e.g., reading in a new curecc file), a different value of gcal should be expected.

Before running setgcal, use the pulse sequence set up by profile to acquire a signal from a known sized object while the gradient is on.

Related:

gcal	Gradient calibration constant (P)
gro	Readout gradient strength in DAC units (P)
profile	Set up pulse sequence for gradient calibration (M)

setgcoil **Update system gradient coil configuration**

Syntax: setgcoil<(file)>

Description: Updates the system gradient coil configuration to correspond to changes in gradient hardware.

Imaging and localized spectroscopy experiments require proper gradient calibration information to properly function. Gradient calibrations (such as the maximum gradient strength, gmax, and rise time, trise) are stored in calibration files found in /vnmr/imaging/gradtables for each gradient hardware option, and specified through the gcoil and sysgcoil parameters. When a new or different gradient set is installed, the configuration parameter sysgcoil must be set to the name of the file in gradtables that describes the new hardware. Because this config operation can be executed only by the user vnmr1, the special function setgcoil has been provided to allow any user to update this particular aspect of the system configuration file.

setgcoil updates the system gradient configuration "permanently" (i.e., until setgcoil is run again or until the system gradient configuration is changed through the config program).

sysgcoil is a system global configuration parameter, and specifies to all users and all experiments the type of gradient hardware installed on the spectrometer. A second parameter, gcoil, is found in all experiment parameter sets, and is saved with the experimental data along with gmax and trise. Once sysgcoil is updated with the setgcoil macro, gcoil in the current experiment is updated as well, and new gradient calibration values are retrieved from the corresponding gradtables file. As different experiments are joined, or new parameter sets retrieved, gcoil and the gradient calibrations are updated in each case to match the new sysgcoil. Therefore, each experiment and all saved data sets retain a record of what gradient hardware was in place at the time of data acquisition.

Arguments: file specifies the name of the gradtables calibration file.

Examples: setgcoil('asg33')

Related:

config	Display current configuration and possibly change it (M)
creategtable	Create new gradient calibration file (isotropic strengths) (M)

gcoil	Current gradient coil (P)
gmax	Maximum gradient strength (P)
sysgcoil	System gradient coil (P)
trise	Gradient rise time (P)
updtgcoil	Update gcoil and gradient calibration parameters (M)

setloop **Set nf and ni values to control arrayed and real-time looping**

Syntax: setloop

Description: Sets the values for the parameters nf and ni to control arrayed and real-time looping.

Loop control in imaging experiments (such as multislice, multiecho, and phase encoding) is set through a series of parameters that the user sets directly (ne, ns, nv, nv2, and nv3). Underlying these parameters are two "lower level" parameters, nf and ni, which are used during pulse sequence execution to determine the mode of data acquisition. setloop manages the values of nf and ni as required to be consistent with the experiment parameters ne, nv, etc.

Two modes of data acquisition are supported in VNMR: "arrayed" and "compressed." The difference is mainly in the timing of the flow of data between host and acquisition computers.

Arrayed data acquisition involves continuous communications between host and acquisition as pulse sequence instructions are sent to the acquisition CPU and data returned to the host Sun for each element in the arrayed experiment. All explicitly arrayed experiments (for example, pw=10,20,30) run in this manner. 2D experiments, including most high-resolution liquids and many imaging experiments, also run as "implicit" arrays, with the array size set by ni. Although the communications between acquisition and host computers are quite fast, a small delay, typically a few msec, is required to accommodate the communications and reinitialization between array elements. Certain fast imaging experiments (such as turboflash, echo planar imaging [EPI], or even conventional multislice) often require loop timing that is on the order of this interelement delay. These experiments use a second mode of data acquisition, the compressed mode.

In compressed data acquisition, a single pulse sequence instruction set is sent to the acquisition computer, which then manages the entire experiment through real-time loops and pulse sequence elements. All data that is accumulated in the real-time loops is retained in the acquisition data memory until the experiment or array element is complete, at which time it is sent back to the host. There is no timing overhead associated with a real-time loop, and extremely short timing intervals can therefore be achieved with the compressed mode. Compressed data acquisition is controlled by the parameter nf, following the single rule that the number of points acquired must be nf*np.

Experiments can be run completely in arrayed acquisition mode, or completely in compressed acquisition mode, or in a combination of the two.

setloop uses the seqcon parameter to determine which acquisition loops, if present, are arrayed and which are compressed. It then computes nf as the product of all compressed loop counts, and sets ni appropriately as either nv in the case of uncompressed phase-encode, or zero in the case of compressed phase-encode.

Each of the parameters ne, ns, nv, nv2, and nv3 have corresponding underscore macros that execute setloop (for example, _ne). setloop is thus a lower level

"management" macro that is automatically run each time one of these parameters is entered, and is not normally and explicitly run by the user. The comprehensive setup macro `imprep` also performs the `setloop` function, so if `imprep` has been executed, there is no need to run `setloop`.

Related:		
	`d0`	Overhead delay between FIDs (P)
	`flashc`	Convert compressed 2D data to standard 2D format (M)
	`imprep`	Set up rf pulses, imaging and voxel selection gradients (M)
	`ne`	Number of echoes to be acquired (P)
	`nf`	Number of FIDs (P)
	`ni`	Number of increments in first indirectly detected dimension (P)
	`ns`	Number of slices to be acquired (P)
	`nv`	Number of phase encode steps for 1st indirectly detected dimension (P)
	`seqcon`	Acquisition loop control (P)

`setof` Measure and save resonance transmitter offset frequency

Syntax: `setof`

Description: Collects a spectrum and determines the resonance frequency of the tallest peak in a spectrum. The corresponding transmitter frequency, `tof`, is then saved in the file `$HOME/vnmrsys/H1offset` for use in imaging experiments. `H1` refers to the value of the current nucleus parameter, `tn`. If the `s2pul` sequence is used to collect data, then `setof` sets the transmitter on the tallest peak and collects a dataset and displays the result, which shows the tallest peak appearing in the center of the spectrum.

Related:		
	`ldof`	Load resonance offset frequency (P)
	`tn`	Nucleus for observe transmitter (P)
	`tof`	Frequency offset for observe transmitter (P)

`setorient` Set imaging orientation Euler angles to match orient

Syntax: `setorient`

Description: Sets the imaging orientation Euler angles to match the `orient` parameter. This is a lower level macro that is not normally directly executed by the operator.

Imaging plane orientation is normally selected through `orient`, or through interactive graphical planning. However, oblique gradient pulse sequence elements use a set of three Euler angle parameters `phi`, `psi`, and `theta`, to determine the exact angular orientation. Each of the three major imaging plane orientations, `trans`, `sag`, and `cor` require a unique set of Euler angles.

`setorient` is automatically executed upon entry of `orient`, and sets the three Euler angles to the appropriate values for the specified orientation.

Related:		
	`orient`	Slice plane orientation (P)
	`phi`	Euler angle for defining imaging plane orientation (P)
	`psi`	Euler angle for defining imaging plane orientation (P)
	`theta`	Euler angle for defining imaging plane orientation (P)

`setgpe` Set phase encode gradient levels and timing

Syntax: `setgpe`

Description: In imaging experiments, automatically computes and sets the phase encode increment and timing, and the indirect dimension “spectral width” associated with each phase encode dimension present.

The `gradient*time` integral for the increment between phase encode levels is governed by the requirement that the spins at the edges of the field-of-view undergo a phase shift of 180°. The phase encode time, `tpe`, is set to `2*trise`, and the phase encode increment is then computed, in G/cm, to satisfy the expression γ`*tpe*lpe*gpe=1`. Some imaging sequences might internally alter the value of `tpe`, with a corresponding change in `gpe`, where timing of the sequence events allows. `setgpe` performs these computations for each phase encode gradient.

A 2D sequence generally has one readout dimension and one phase-encode dimension, described by the parameters gpe, `sw1`, and tpe. A second or third phase encode dimension is described by the triad of parameters `gpe`, `sw2`, `tpe2`, and `gpe3`, `sw3`, `tpe3`, respectively. The spectral width associated with each phase encode dimension is computed as 1/tpe (or 1/tpe2, etc.), and has no physical significance. sw1 is present to provide compatibility with analytical 2D NMR data processing and display routines in VNMR. The comprehensive setup macro `imprep` incorporates the functions of `setgpe`, so that `setgpe` is not normally directly executed by the operator.

Related:

`gpe`	Phase encoding gradient increment in DAC units (P)
`imprep`	Set up rf pulses, imaging and pulse power levels (M)
`nv`	Number of phase encode steps for1st indirectly detected dim. (P)
`setgro`	Set readout gradient strength and spectral width (M)
`setgss`	Set slice-selection gradient strength (M)
`sw1`	Spectral width in first indirectly detected dimension (P)
`tpe`	Duration of the phase encoding gradient pulse (P)

`setgro` Set readout gradient strength and spectral width

Syntax: `setgro<(readout_gradient|level)>`

Description: In imaging experiments, automatically computes and sets the readout gradient strength, `gro`, and spectral width, `sw`, for the readout dimension, consistent with the field of view, `lro`.

The relationship between gradient strength, field of view, and spectral width is governed by the principle that the spins at the edges of the field of view must undergo a phase shift of 180° during the dwell time between successive sampling of points (Nyquist sampling frequency), following the expression `sw=`γ`*lro*gro`. In its automatic mode, `setgro` attempts to balance two opposing factors in choosing the readout gradient strength: too low a value of `gro` results in large chemical shift displacement artifacts in the resulting image. Too high a value of `gro` requires a large spectral width, and therefore a large audio filter bandwidth, resulting in increased noise and reduced signal-to-noise in the resulting image.

In both “manual” and automatic modes, `setgro` uses the current values for number of points `np` and field of view `lro`. `np` can be subsequently altered without the need to re-run `setgro` (or `imprep`), but any change of `lro` must be followed by execution of `setgro` or `imprep` to recompute other dependent parameters. The comprehensive setup macro `imprep` incorporates the functions of `setgro`, so `setgro` is not normally directly executed by the operator except to override the value of `gro` selected by `imprep`.

Arguments: `readout_gradient` is a specific value entered, in G/cm, as a numeric argument. When this value is entered, `setgro` can be used in manual mode to explicitly set the readout gradient.

`level` is a real number that is interpreted as a gradient level in gauss/cm. Provided that the number ranges from `0` to `gmax`, `setgro` sets `gro` to the specified value, and computes and sets the corresponding values of `sw` and `at`.

Examples:
```
setgro
setgro(3.5)
```

Related:

`at`	Acquisition time (P)
`gro`	Readout gradient strength (P)
`imprep`	Set up rf pulses, imaging and pulse power levels (M)
`lro`	Field of view size for readout axis (P)
`np`	Number of data points (P)
`setgpe`	Set phase encode gradient levels and timing (M)
`setgss`	Set slice-selection gradient strength (M)
`sw`	Spectral width in directly detected dimension (P)

`setgss` Set slice-selection gradient strength

Syntax: `setgss<(gradient_parameter,thickness_parameter)>`

Description: In imaging experiments, automatically computes and sets the value of any slice or voxel selection gradient, in G/cm, to achieve the required slice or voxel thickness. The comprehensive setup macro `imprep` incorporates the functions of `setgss`, so `setgss` is not normally entered by the operator.

`setgss` relies on the list parameters `fliplist`, `plist`, `patlist`, and `sslist` to provide the correspondence between the selective gradient and the rf flip angle, pulse length, and shape. The list parameters must be present with appropriate entries, and the specified rf shape file must exist in `shapelib` with the proper header information.

Gradient strength for a slice or voxel-selective event is determined from the relationship `gss=BW/(γ*thk)`, where `gss` is the gradient strength, `BW` is the rf pulse bandwidth, and `thk` is the slice or voxel thickness.

`setgss` uses the rf pulse bandwidth extracted from the rf shape file in `shapelib`, together with the slice or voxel thickness, to compute and assign the required gradient strength, in G/cm. If more than one rf pulse is used during a sequence for a slice selection operation on a given axis (such as in a spin-echo imaging sequence, where both the 90° and 180° pulses are slice selective on a single axis, with slice gradient level specified by `gss`), the effective bandwidth of each is determined and the smallest bandwidth is used to compute `gss`.

If the rf pulse or pulses found in `plist` are not frequency selective, `setgss` issues an error message and exits. If the slice or voxel thickness found in the designated thickness parameter is too small for the maximum gradient strength of the system, the thickness value is reset to its minimum possible value consistent with `gmax`.

Arguments: `gradient_parameter` is the gradient strength parameter.

`thickness_parameter` is the slice or voxel thickness parameter.

Examples:
```
setgss
setgss('gss','thk')
setgss('gvox1','vox1')
```

Related:

fliplist	Flip angle list (P)
patlist	Pulse shape parameter list (P)
sslist	Gradient parameter names list (P)
gmax	Maximum gradient strength (P)
gss	Slice selection gradient strength (P)
imprep	Set up rf pulses, imaging and pulse power levels (M)
plist	Pulse length parameter list (P)
setgpe	Set phase encode gradient levels and timing (M)
setgro	Set readout gradient strength and spectral width (M)

setvgrad — Set voxel-selection gradient strengths

Syntax: `setvgrad`

Description: In localized spectroscopy experiments, automatically computes and sets the voxel selection gradients, in G/cm, to achieve the required voxel dimensions.

`setvgrad` calls the macro `setgss` for each of the three voxel axes, using the parameters `gvox1`, `gvox2`, and `gvox3` for the gradient strength parameters and `vox1`, `vox2`, and `vox3` for the voxel dimension parameters. If any of the voxel dimensions are arrayed, `setvgrad` configures the array parameter to give the proper diagonally arrayed experiment.

Related:

gvox1, gvox2, gvox3	Gradient strength for voxel selection (P)
imprep	Set up rf pulses, imaging and pulse power levels (M)
setgss	Set slice-selection gradient strength (M)
vox1,vox2, vox3	Voxel dimensions (P)

steam — Retrieve parameters for STEAM imaging experiment

Syntax: `steam`

Description: Retrieves the standard parameters for the STEAM imaging experiment from `/vnmr/parlib`.

tabgen — Create AP table for k-space order (M)

Syntax: `tabgen`

Description: In imaging experiments, creates an AP table for the k-space (phase-encode) order.

Conventional imaging experiments generally follow a monotonic phase encode order that begins at one extreme and progresses monotonically through zero to the opposite extreme. For example, the multipliers for the phase encode step might be –64,–63,–62,...,–2,–1,0,1,2,...,62,63 for an imaging experiment with 128 phase encode levels. VNMR's pulse sequence capabilities allow the use of a k-space order that is nonmonotonic through the use of external AP tables (simple text files with a list of integer values). `tabgen` can be used to create one of these tables for either a monotonic progression or a centrically ordered progression (centric order starts at zero and progresses to the extremes in an alternating positive and negative fashion (e.g., 0,1,–1,2,–2,3,–3,...).

`tabgen` prompts for the type of order, the number of steps, and a file name for the resulting table. Imaging data acquired in nonmonotonic order must first be

processed with the `tabc` routine, because `ft2d` expects data to have been acquired in monotonic phase encode order.

Related:	`ft2d`	Fourier transform 2D data (C)
	`petable`	Table name for tablib (P)
	`tabc`	Convert data from table specified order to monotonic order (C)

`tpwrcal` Set up imaging power calibration

Syntax: `tpwrcal(start,end)`

Description: Sets up a simultaneous array of the parameters `tpwr1` and `tpwr2` (typically used in imaging sequences as the excitation and refocusing pulse powers) for imaging power calibration. This array provides a convenient method of calibrating pulse powers using the readout profile.

`tpwr2` is arrayed in steps of one over this range, and a `tpwr1` array is also constructed with a difference of six units between each `tpwr1` element and the corresponding `tpwr2` element (12 units for older SISCO VXR and Unity systems). The difference of 6 dB in power gives a factor of two in pulse amplitude, which is appropriate for any spin echo sequence using 90° and 180° pulses. The resulting arrayed data can be used to create a new pulse calibration entry by choosing the power value that gives the profile with the largest amplitude.

Arguments: `start` is the first value for the `tpwr2` part of the arrayed pairs. The starting value for `tpwr2` is 6 less than `tpwr2_start`.

`end` is the last value for the `tpwr2` part of the arrayed pairs. The ending value for `tpwr2` is 6 less than `end_tpwr`.

Examples: `tpwrcal(46,51)` produces this data:

```
tpwr1 = 40,41,42,43,44,45
tpwr2 = 46,47,48,49,50,51
array = '(tpwr1,tpwr2)'
```

Related:	`array`	Parameter order and precedence (P)
	`setarray`	Set up a parameter array (M)
	`tpwr, tpwr1 – tpwr5`	Pulse power levels (P)

`updtgcoil` Update gcoil and gradient calibration parameters

Applicability: Systems with three-axis gradients.

Syntax: `updtgcoil`

Description: Updates the `gcoil` parameter and gradient calibration parameters in imaging experiments.

`updtgcoil` is automatically called (if `gcoil` exists in the new parameter set) when a new parameter set is loaded, or when an experiment is joined, to update the experiment parameters `B0`, `gcoil`, `gmax`, and `trise` to match the calibration values specified by the configuration parameter `sysgcoil`.

`updtgcoil` first checks to see that gradients are present on the system, then (if `sysgcoil` is set to a value other than `'none'`) assigns the value of `sysgcoil` to `gcoil`, which forces the gradient calibration parameters to be updated with the values found in the corresponding gradtables entry. If `gcoil` does not exist, `updtgcoil` will create it.

updtgcoil also computes the system field strength and assigns this to the parameter B0. It is automatically called by the rt macro, and by the jexp macro, and is not normally directly executed by users.

Related:

B0	Magnet main static field (P)
gcoil	Current gradient coil (P)
gmax	Maximum gradient strength (P)
jexp	Join existing experiment (C)
rt	Retrieve FIDs (M)
sysgcoil	System gradient coil (P)
trise	Gradient rise time (P)

A.3 Macros for Planning Experiments

Use the macros in this section when planning experiments.

addpss — Shift a set of multislice positions

Syntax: addpss<(shift)>

Description: Shifts a set of multislice positions by adding a constant value to all elements of the pss array. addpss adds a constant value to each element of the pss array to shift a set of multislice positions a fixed distance.

Arguments: shift specifies the amount of shift, in cm. The default is the macro prompts for a value.

Examples:
```
addpss
addpss(2)
```

Related:

plan	Interactive slice and voxel selection (M)
pss	Slice position (P)

drawslice — Draw a set of planned target imaging slices on scout image

Syntax: drawslice

Description: Displays the positions of a newly planned set of multislice planes on the scout image. drawslice is called by the Compute Target button in the slice planning menu, and is not normally executed from the command line. However, because it is a macro, it is possible to change the color used to draw the slice positions.

drawslice uses the coordinates of a pair of points found in the parameter t_mark, which must have previously been selected using the Mark button in the slice planning menu. These two points define the orientation of the new target imaging plane.

See also: "Target Parameters," page 341

Related:

drawvox	Draw outline of a planned target voxel on scout image (M)
plan	Interactive slice and voxel selection (M)

drawvox — Draw outline of a planned target voxel on scout image

Syntax: drawvox

Description: Displays the outline of a newly planned voxel (or multiple voxels) on the scout image. drawvox is called by the Compute Target button in the voxel planning

menu, and is not normally executed from the command line. However, because it is a macro, it is possible to change the color used to draw the voxel position.

`drawvox` uses the box coordinates found in the parameter `t_mark`, which must have previously been selected using the Mark button in the voxel planning menu.

See also: "Target Parameters," page 341

Related:

`drawslice`	Draw a set of planned target imaging slices on scout image (M)
`plan`	Interactive slice and voxel selection (M)

`location` Display spatial coordinates at a point in an image

Syntax: `location`

Description: Computes and displays the position of a point in an image defined by the intersection of the horizontal and vertical cursors. Two sets of coordinates are computed:

- Logical reference frame coordinates corresponding to the readout, phase-encode.
- Slice select axes; and the absolute magnet frame coordinates corresponding to the laboratory X, Y, and Z axes.

Related:

`log_mag`	Convert spatial coordinates (M)

`log_mag` Convert spatial coordinates

Syntax: (From UNIX) `log_mag phi psi theta x y z`

Description: Converts spatial coordinates in the logical reference frame to spatial coordinates in the magnet reference frame. `log_mag` is an executable macro command in `/vnmr/bin`. It must be executed from a UNIX shell or called from a VNMR macro by the `shell` command.

Arguments: `phi`, `psi`, `theta` are the coordinates of a point in the logical imaging reference frame (the coordinate system defined by the readout, phase encode, and slice select axes) and the Euler angles that define the orientation of the logical frame:

- `phi` is the angular rotation of the image plane about a line normal to the image plane.
- `psi` is formed by the projection of a line normal to the imaging plane onto the magnet XY plane, and the magnet Y axis.
- `theta` is formed by the line normal to the imaging plane, and the magnet Z axis.

`x`, `y`, `z` are the magnet reference frame coordinates that are returned to standard output, which is printed to the calling window unless picked up as return arguments to the VNMR `shell` command.

Related:

`location`	Display spatial coordinates at a point in an image (M)
`orient`	Slice plane orientation (P)
`phi`	Euler angle for defining imaging plane orientation (P)
`psi`	Euler angle for defining imaging plane orientation (P)
`theta`	Euler angle for defining imaging plane orientation (P)

plane_decode **Compute new imaging plane orientation and position**

Syntax: (From UNIX) `plane_decode psi phi theta x1 y1 z1 x2 y2 z2`

Description: Computes the orientation and position for a new imaging plane using the coordinates of two points on a scout image. `plane_decode` takes the coordinates of a pair of points in the logical imaging reference frame and the Euler angles that define the logical frame orientation, and returns the orientation and position of an imaging slice that contains those points and is perpendicular to the scout image plane. `plane_decode` is an executable macro command in `/vnmr/bin`.

Arguments: `phi` is the angular rotation of the image plane about a line normal to the image plane.

`psi` is formed by the projection of a line normal to the imaging plane onto the magnet XY plane, and the magnet Y axis.

`theta` is formed by the line normal to the imaging plane, and the magnet Z axis.

`x1`, `y1`, `z1`, `x2`, `y2`, `z2` are the orientation and position of the new imaging plane returned from `plane_decode`.

Related:

`orient`	Slice plane orientation (P)
`phi`	Euler angle for defining imaging plane orientation (P)
`psi`	Euler angle for defining imaging plane orientation (P)
`pss`	Slice position (P)
`theta`	Euler angle for defining imaging plane orientation (P)

plan **Interactive slice and voxel selection**

Syntax: `plan`

Description: Displays a menu of interactive planning choices used to define new slice or voxel targets for imaging and localized spectroscopy experiments. The menu allows graphical selection of new target slice or voxel positions and orientations from a scout imaging experiment, and transfer of this information to the target imaging or localized spectroscopy experiment.

Related:

`transfer`	Move field-of-view information to a target experiment (M)

slicemark **Store marked positions for planning target imaging planes**

Syntax: `slicemark<('reset')>`

Description: Stores the locations of points selected during the planning of new imaging plane positions and orientations in the parameter `t_mark`. `slicemark` is called by the Mark button in the Slice planning menu and is not normally executed from the command line.

Arguments: `'reset'` is a keyword to clear any previously marked positions by zeroing `t_mark`.

See also: “Target Parameters,” page 341.

Related:

`plan`	Interactive slice and voxel selection (M)

sliceorder **Reorder slice position list**

Syntax: `sliceorder<('a'|'d'|'i')>`

Description: Reorders the list of physical slice positions, pss, in ascending, descending, or alternating odd and even order.

Alternating order is often used for multislice excitation to separate physically adjacent slices in time to reduce saturation effects. For example, the result of `sliceorder('a') pss=-3,-2,-1,0,1,2,3` is `pss=-3,-1,1,3,-2,0,2`. The adjacent slices `-1` and `-2` are separated by three time intervals instead of just one.

Arguments: `'a'` is a keyword to list physical slice positions in alternating order. This is the default.

`'d'` is a keyword to list physical slice positions in descending order.

`'i'` is a keyword to list physical slice positions in ascending order.

Examples:
```
sliceorder
sliceorder('d')
```

Related:

pss	Slice position (P)

sliceplan — Compute slice position and orientation for target imaging plane

Syntax: `sliceplan`

Description: Computes the slice position and orientation for a new target imaging plane from a pair of marked positions found in the t_mark parameter. `sliceplan` is called by the Compute Target button in the Slice planning menu, and is not normally executed from the command line.

`sliceplan` first determines the coordinates of the two marked points in the scout imaging plane reference frame, then calls a separate program to compute the orientation and position of the new target slice. The computed results are stored in the target planning parameters `t_pss`, `t_thk`, `t_phi`, `t_psi`, and `t_theta` for later transfer to a new target experiment.

See also: "Target Parameters," page 341

Related:

plan	Interactive slice and voxel selection (M)
slicemark	Store marked positions for planning target imaging planes (M)
voxplan	Compute position and orientation for new target voxel (M)

transfer — Move field-of-view information to a target experiment

Syntax: `transfer(type<,scout_exp>,target_exp)`

Description: Transfers planned slice or voxel position information from a scout experiment to a target experiment. `transfer` takes the values found in the appropriate t_ parameters and places them in the corresponding parameters in the target experiment. These values are normally selected through interactive graphical planning. `transfer` is called by the Transfer buttons in the Slice planning and Voxel planning menus and is not normally executed from the command line.

`transfer` uses predefined sets of parameter names to extract the required slice or voxel values from the scout experiment. For example, the transfer of slice planning information takes the values of `t_phi`, `t_psi`, `t_theta`, `t_pss`, and `t_thk` from the scout experiment and places them in phi, psi, theta, pss, and thk in the new target experiment. The parameters resto and rfcoil are also transferred.

Arguments: `type` is a keyword that specifies the transfer type: `'s'` for slice or `'v'` for voxel.

`scout_exp` is the experiment number (1 to 9) of the scout experiment. The default is that the current experiment is the scout experiment.

`target_exp` is the experiment number (1 to 9) of the target experiment. If only one numerical argument follows the `type` argument, the current experiment is the scout experiment and the numerical argument is the experiment number of the target experiment.

Examples:
```
transfer('s',6)
transfer('v',2,7)
```

See also: "Target Parameters," page 341

Related:

mp	Move parameters between experiments (C)
mvfov	Move the field-of-view from one experiment to another (M)
plan	Interactive slice and voxel selection (M)
phi	Euler angle for defining imaging plane orientation (P)
psi	Euler angle for defining imaging plane orientation (P)
resto	NMR resonance offset frequency (P)
rfcoil	RF pulse calibration identity (P)
theta	Euler angle for defining imaging plane orientation (P)
thk	2D imaging plane slice thickness (P)

voxmark — Store marked positions for planning target voxels

Syntax: `voxmark<('reset')>`

Description: Stores the locations of points selected during the planning of new voxel positions and dimensions in the parameter `t_mark`. `voxmark` is called by the Mark button in the Voxel planning menu, and is not normally executed from the command line.

Arguments: `'reset'` is a keyword to clear any previously marked positions by zeroing `t_mark`.

See also: "Target Parameters," page 341

Related:

plan	Interactive slice and voxel selection (M)

voxplan — Compute position and orientation for new target voxel

Syntax: `voxplan`

Description: Computes the position, dimensions, and orientation for a new target voxel from a set of marked positions found in the `t_mark` parameter. Multiple voxels previously selected with the voxel planning Mark button are properly handled by `voxplan`, resulting in an array of voxel positions and dimensions. `voxplan` is called by the Compute Target button in the Voxel planning menu, and is not normally executed from the command line,

`voxplan` stores its computed results in the target planning parameters `t_pos1`, `t_pos2`, `t_pos3`, `t_vox1`, `t_vox2`, `t_vphi`, `t_vpsi`, and `t_vtheta` for later transfer to a new target experiment. The out-of-plane voxel dimension `t_vox3` must be selected separately with the Set vox3 button in the Voxel planning menu.

See also: "Target Parameters," page 341

Related:

plan	Interactive slice and voxel selection (M)
sliceplan	Compute slice position and orientation for target imaging plane (M)
voxmark	Store marked positions for planning target voxels (M)

A.4 Commands and Macros for Processing and Display

Use the macros in this section to process and display data and graphics.

dconi **Interactive 2D data display (C)**

Syntax: `dconi<(options)>`

Description: Interactively adjusts various 2D data displays. The `dconi` program can accommodate any data set that can be displayed by `dcon`, `dpcon`, and `ds2d`, including 2D FIDs, interferograms, 2D spectra, planes from 3D data sets, and images. These data sets are generated by the commands `df2d`, `ft1d`, `ft2d`, and `ft3d`.

Arguments: `options` can be any of the following (note that the `dconi` parameter is also available to control the `dconi` program display):

- `'dcon'` is a keyword to display a color intensity map; this is the default mode, but `'dcon'` is provided for compatibility with certain macros. If `'dcon'` is the first argument, it can be followed by any of the keywords `'linear'`, `'phcolor'`, `'avcolor'`, `'gray'`, and `'noaxis'`; all of these keywords have the same meaning as when used with the `dcon` command.
- `'dpcon'` is a keyword to display a true contour plot. If `'dpcon'` is the first argument, it can be followed by any of the keywords `'pos'`, `'neg'`, and `'noaxis'`, and then followed by values for `levels` and `spacing`. All of these options have the same meaning as when used with the `dpcon` command.
- `'ds2d'` is a keyword to display a stacked plot in whitewash mode (after the first spectra, each spectra is blanked out in regions in which it is behind an earlier spectra). If `'ds2d'` is the first argument, it can be followed by any of the keywords `'nobase'`, `'fill'`, `'fillnb'`, and `'noaxis'`. All of these keywords have the same meaning as used with `ds2d`.
- `'again'` is a keyword to make `dconi` identify which display mode is currently being used and redraw the screen in that mode. This option is useful when writing VNMR menus.
- `'restart'` is a keyword to activate `dconi` without redrawing the 2D data set. This action causes `dconi` to make sure that 2D data is already displayed.
- `'toggle'` is a keyword to toggle between the cursor and box modes.
- `'trace'` is a keyword to draw a trace above the spectrum.
- `'expand'` is a keyword to toggle between the expand and full views of the spectrum.
- `'plot'` is a keyword to plot a projection or a trace.
- `'hproj_max'` is a keyword to do a horizontal projection of the maximum trace.
- `'hproj_sum'` is a keyword to do a horizontal projection of the sum of all traces.
- `'vproj_max'` is a keyword to do a vertical projection of the maximum trace.
- `'vproj_sum'` is a keyword to do a vertical projection of the sum of all traces.

Examples:
```
dconi
dconi('dcon','gray','linear')
dconi('dpcon')
```

dgm **Display dg parameter groups menu (M)**

Syntax: `dgm`

Description: Displays a menu that allows selection of all `dg` parameter groups in an experiment. The primary parameters of any imaging experiment can be displayed in the text window with the `dg` command. Most secondary parameter groups, such as `dg1` and `dgs`, are found in each imaging experiment, along with several other specialized parameter groups. These additional parameter groups allow the display, for example, of all predefined gradient parameters, or all predefined rf pulse parameters, etc., although some of the displayed parameters are unused in any given experiment and have values set to zero or null-string.

`dgm` allows menu selection of the various dg screens in any experiment by searching for all parameter names that begin with the two letters 'dg', and presenting a menu of all such names. To display any of these parameter groups, select the button with the desired name or description. The Print button in the dgm menu prints the currently displayed parameter group.

Related: `dg` Display group of acquisition/processing parameters (C)

disp3d **Display 3D data (U)**

Syntax: (From UNIX) `disp3d <fdf_file>`

Description: Displays a 3D FDF (Flexible Data Format) file or a raw 8-bit 3D data file with no header. Compatible FDF files are produced by `ft3d` with the `'fdf'` option (or by default if `appmode='imaging'`).

FDF data can also be loaded either by entering the file name as an argument to `disp3d` or by typing the file name into the File field in the `disp3d` control panel and clicking the Load button. If the FDF data word size is larger than 8 bits, the data are scaled and truncated to 8 bits for display. Raw data files can only be loaded from the control panel.

Besides the file name, the user must enter the size of the data matrix in the fast, medium, and slow dimensions in the Data size field. Typically, these would be the values `fn/2`, `fn1/2`, and `fn2/2`, respectively.

Furthermore, the desired size of the image in screen pixels—also in the fast, medium, and slow dimensions—must be entered in the Display size fields. Typically, these values would be near 100 and the relative ratio of the parameters `lro`, `lpe`, and `lpe2`, respectively.

After loading the data, a 3D volume appears in the display panel.

Arguments: `fdf_file` is the name of a file containing FDF data.

Related:

`appmode`	Application mode (P)
`fn`	Fourier number in directly detected dimension (P)
`fn1`	Fourier number in 1st indirectly detected dimension (P)
`fn2`	Fourier number in 2nd indirectly detected dimension (P)
`ft3d`	Perform a 3D Fourier transform on a 3D FID data set (M,U)
`lpe`	Field of view size for phase encode axis (P)

lpe2	Field of view size for 2nd phase-encode axis (P)
lro	Field of view size for readout axis (P)

dmi **Transform and display multiple images in VNMR graphics window (M)**

Syntax: `dmi`

Description: Transforms and displays a series of multiple images from an arrayed, multislice or multiecho imaging experiment in the VNMR graphics window. Because the resulting image display is noninteractive, changes in expansion, vertical scale, window and level must be made on a single interactive display before executing dmi. The layout and size of the images are optimized to maximize the image display on the usable graphics region. Images can be displayed in either the `trace='f1'` or the `trace='f2'` mode, in either full or zoomed modes. To force VNMR to use the entire graphics window, set the `wysiwyg` parameter to 'n' before running dmi.

Related:

imconi	Display 2D data in interactive grayscale mode (M)
imconn	Display 2D data without erasing the screen (M)
svib	Generate and save images as Image Browser-compatible FDF files (M)
wysiwyg	Set plot display or full display (P)

dpss **Display current pss slice positions list (M)**

Syntax: `dpss`

Description: Displays the current list of slice positions found in the parameter `pss`. The list of slice positions in a multislice imaging experiment is stored in the arrayed parameter pss. An acquisition parameter arrayed in this way normally results in an arrayed experiment, in which each slice acquisition is treated as a separate array element. pss is configured through its protection bits to prevent the execution of a conventional arrayed acquisition, and instead to allow a “compressed” multislice acquisition that uses the arrayed pss values to specify the slice positions in a compressed multislice loop. This unusual parameter protection also prevents `da` from displaying its values, although a display of the array list can be forced by specifying the name of the parameter in an argument to `da` (e.g., `da('pss')`). `dpss` is exactly this macro, and is provided to allow the list of `pss` values to be easily viewed.

Related:

da	Display acquisition parameter arrays (C)
pss	Slice position (P)
setprotect	Set protection mode of a parameter (C)

dssh **Display stacked spectra horizontally (C)**

Syntax: `dssh<(<start,finish<,step>><,options>)>`

Description: Displays one or more spectra horizontally. When a single spectrum is displayed, integral display is controlled by the parameter `intmod`., which can have the following values:

- `intmod='off'` turns off the integral display.
- `intmod='full'` displays the entire integral.
- `intmod='partial'` displays every other integral region.

For arrayed 1D spectra or for 2D spectra, a particular trace can be viewed by supplying the index number as an argument. For 2D data sets, spectra can be displayed from either the f_1 or f_2 domain by setting the parameter `trace` equal

to `'f1'` or `'f2'`, respectively. After entering `ft1d`, interferograms can be viewed by setting `trace='f1'` and then entering `dss`. Multiple spectra can be displayed by supplying indexes of the first and last spectra.

The position of the first spectrum is governed by the parameters `wc`, `sc`, and `vp`. For 1D data, subsequent spectra are positioned relative to the preceding spectrum by the parameters `vo` (vertical offset) and `ho` (horizontal offset). For 2D data, `ho` defines the total horizontal offset between the first and last spectrum. Also for 2D data, `vo` is inactive while the parameter `wc2` defines the total vertical offset between the first and last spectrum. To display spectra horizontally, the command `dssh` causes `vo` to be set to zero and for `ho`, `sc`, and `wc` to be adjusted to fill the screen from left to right with the entire array.

The parameter `cutoff`, if it exists and is active, defines the distance above and below the current vertical position `vp` at which peaks are truncated. By arraying `cutoff` to have two different values, the truncation limits above and below the current vertical position may be controlled independently. For example, `cutoff=50` truncates peaks at `vp+50` mm and `vp–50` mm, and `cutoff=50,10` truncates peaks at `vp+50` mm and `vp–10` mm.

Arguments: `start` is the index of the first spectra when displaying multiple spectra. It is also the index number of a particular trace to be viewed when displaying arrayed 1D spectra or 2D spectra.

`finish` is the index of the last spectra when displaying multiple spectra.

`step` is the increment for the spectral index when displaying multiple spectra. The default is 1.

`options` can be any of the following:

- `'all'` is a keyword to display all of the spectra.
- `'int'` is a keyword to only display the integral, independently of the value of the parameter `intmod`.
- `'dodc'` is a keyword that causes all spectra to be drift corrected independently.

Examples: `dssh(1,3)`

See also: *User Guide: Liquids NMR*

Related:

`cutoff`	Data truncation limit (P)
`dss`	Display stacked spectra (C)
`dssa`	Display stacked spectra automatically (C)
`dssan`	Display stacked spectra automatically without erasing (C)
`dsshn`	Display stacked spectra horizontally without erasing (C)
`dssn`	Display stacked spectra without screen erase (C)
`dsww`	Display spectra in whitewash mode (C)
`ft1d`	Fourier transform along f_2 dimension (C)
`ho`	Horizontal offset (P)
`intmod`	Integral display mode (P)
`pl`	Plot spectra (C)
`plww`	Plot spectra in whitewash mode (C)
`sc`	Start of chart (P)
`sc2`	Start of chart in second direction (P)
`trace`	Mode for 2D data display (P)
`vo`	Vertical offset (P)
`vp`	Vertical position of spectrum (P)
`wc`	Width of chart (P)
`wc2`	Width of chart in second direction (P)

dssl **Label stacked spectra display (M)**

Syntax: `dssl<(options)>`

Description: Displays a label for each spectrum in a set of stacked spectra.

Note that with `wysiwyg='n'`, labels can appear at incorrect vertical positions. `$scale` is used in `dssl` to compensate for a bug in write positioning. Positions were empirically determined for a large screen, and are not guaranteed to be correct for all displays.

Arguments: The default label is an integer value starting with 1 and extending up to the number of spectra in the display. Several options are available to control the position of the displayed index relative to each spectrum. More than one nonconflicting option can be entered. Positional options are:

- `above'` displays a label just above the baseline of each spectrum.
- `'below`' displays a label just below the baseline of each spectrum
- `'center'` displays start of a label horizontally at the center of each spectrum.
- '`left'` displays start of a label horizontally at the left edge of each spectrum.
- `'right'` displays start of a label horizontally at the right edge of each spectrum.
- `'top'` displays a label at the top of the graphics screen.
- `'bottom'` displays a label at the bottom of the graphics screen.
- `'list='` displays values stored in an arrayed processing parameter, such as intensity, integral, time, frequency, etc. An arrayed processing parameter can be created with the `setgroup` and `setprotect` commands from any acquisition parameter, and used to store a list of values entered on the command line or with any data analysis macro.

`'list=xyz'` produces a display of the values contained in the arrayed parameter `xyz`. This can be used to force `dssl` to display the arrayed values of one of the parameters in a multiple arrayed parameter experiment.

- `'format=abc'` uses the format `abc` to control the display of each label. For example, `dssl('value','format=%.2f')` forces each label to be displayed with two figures to the right of the decimal.
- `'value'` can be used in addition to any positional arguments to produce a display of the values of each array element instead of an integer index (only a single arrayed parameter is supported; `dssl('value')` fails if multiple arrayed parameters are present).
- `dssl('value','format=%3.1 sec')` results in labels of the form “8.3 sec”.

Examples:

```
dssl
dssl('top','left')
dssl('value','format=%3.1f sec')
```

Related:

	`dss`	Display stacked spectra (C)
	`write`	Write formatted text to a device (C)
	`wysiwyg`	Set plot display or full display (P)

ecctool **Open eccTool window (M)**

Applicability: Systems with computer-controlled analog eddy current compensation.

Syntax: `ecctool`

Description: Opens the eccTool window to adjust eddy current compensation parameters.

`eff_echo` **Effective echo position in EPI experiments (P)**

Applicability: Systems with echo planar imaging (EPI) capabilities.

Description: Refers to the echo showing the highest signal in an EPI echo-train. The readout gradient dephaser is adjusted so that the maximum signal occurs at `eff_echo`.

Values: Usually set to `nv/2`.

Related: `nv` Number of phase encode steps for 1st indirectly detected dim. (P)

`epift` **Process and display image in EPI experiments (M)**

Applicability: Systems with echo planar imaging (EPI) capabilities.

Syntax: `epift(index)`

Description: Processes and displays an image in array number `index`. The first data array must contain the reference scan. The phase correction information saved in the file `phasemap` is used to correct phase errors in EPI data. `phasemap` must be present in the current experiment directory. Use `dconi` to view the data.

Arguments: `index` is the array number of the image.

Related:

`dconi`	Interactive 2D data display (C)
`epiph`	Generate phase correction map in EPI experiments (M)
`pcmapapply`	Apply phase correction map to data in EPI experiments (C)

`epiph` **Generate phasemap file in EPI experiments (M)**

Applicability: Systems with echo planar imaging (EPI) capabilities.

Syntax: `epiph`

Description: Generates the `phasemap` file from the EPI reference scan. The file is generated in the current experiment directory for EPI processing. The first data array must correspond to the reference scan, which is collected with the phase-encode gradient turned off `(image=0)`.

Related:

`episet`	Set up parameters for EPI experiments (M)
`image`	Control phase encoding gradient in EPI experiments (P)
`pcmapgen`	Generate phase correction map in EPI experiments (M)

`epirs` **Reverse spectral data in EPI experiments (C)**

Applicability: Systems with echo planar imaging (EPI) capabilities.

Syntax: `epirs`

Description: Reverses spectral data. It is used by `epift`.

Related: `epift` Process and display images in EPI experiments (M)

`epirun` **Collect, process, and display EPI data (M)**

Applicability: Systems with echo planar imaging (EPI) capabilities.

Syntax: `epirun`

Description: Collects, process, and displays EPI data. It is used to obtain a single EPI image. The `phasemap` file must be present in the current experiment directory.

Related:

`epiph`	Generate phasemap file in EPI experiments (M)
`episet`	Set up parameters for EPI experiments (M)

`episet` Set up parameters for EPI experiments (M)

Applicability: Systems with echo planar imaging (EPI) capabilities.

Syntax: `episet`

Description: Collects an EPI dataset with the phase-encode gradient turned off (`image=0`). It optimizes parameters for EPI, collects a reference scan, and allows you to adjust the gradient parameters `groa` and `grora` and the timing parameter `tep`. The `phasemap` file is generated in the current experiment directory.

Related:

`epiph`	Generate phasemap file in EPI experiments (M)
`groa`	Readout gradient adjuster in EPI experiments (P)
`grora`	Readout dephasing gradient adjuster in EPI experiments (P)
`image`	Control phase encoding gradient in EPI experiments (P)
`tep`	Post-acquisition delay in EPI experiment (P)

`episs` Load default parameters

Applicability: Systems with echo planar imaging (EPI) capabilities.

Syntax: `episs`

Description: Loads the default parameters for single-shot EPI from the default parameter directory

`episvib` Save EPI images in FDF for Image Browser (M)

Applicability: Systems with echo planar imaging (EPI) capabilities.

Syntax: `episvib`

Description: Saves images in Flexible Data Format (FDF) for viewing with Image Browser. The first image in an arrayed dataset must contain the reference scan. This scan must be acquired with the phase encode gradient turned off.

Related:

`browser`	Start Image Browser application (U)

`explib2` Display list of current experiments in VNMR text window (M)

Syntax: `explib2`

Description: Displays a summary list of the available experiments, similar to `explib`, in the text window. For each experiment, the experiment number, name of the pulse sequence, and the first part of the text file are displayed. There are three main differences between the macros `explib2` and `explib`:

- `explib2` is a macro, which can be modified by users, while `explib` is a VNMR command.
- `explib2` is somewhat faster than `explib`, primarily because it does not obtain and display the size of each experiment in kilobytes.
- `explib2` does not display any acquisition status information, such as queued experiments, as does explib.

Related:

`explib`	Display experiment library (M)

filter **Set apodization parameters to give Gaussian LP filter for wft2d (M)**

Syntax: `filter(weighting_value)`

Description: Computes the Gaussian weighting parameters `gf`, `gfs`, `gf1`, and `gfs1` to give a Gaussian low-pass smoothing filter for the `wft2d` command.

Arguments: `weighting_value` specifies the degree of weighting, and results in a reduction at the edge of the data approximately equal to the argument value, in dB. The higher the value, the more the weighting and apparent smoothing, smaller values give less apodization and apparent smoothing. A weighting value of zero turns off the Gaussian weighting parameters.

Examples: `filter(10)`

Related:

`gf`	Gaussian function in directly detected dimension (P
`gf1`	Gaussian function in 1st indirectly detected dimension (P)
`gfs`	Gaussian function in directly detected dimension (P)
`gfs1`	Gaussian shift const. in 1st indirectly detected dimension (P)
`wft2d`	Weight and Fourier transform 2D data (C)

findpw **Measure 180° pulse; update pulsecal database (M)**

Syntax: `findpw`

Description: Measures a 180° pulse and updates the `pulsecal` database. `findpw` automatically determines the maximum and minimum signal from a set of ten, predefined pulse lengths and enters the calibration values into the `pulsecal` database. The `s2pul` sequence should already be loaded and running.

Before the new pulse parameters are entered into the `pulsecal` database, the results are displayed on the screen and you are prompted for a response. When you type `'y'`, you are asked for a file name, then the `pulsecal` database is updated.

Arguments: `start_pw_value` specifies the starting `pw` value.

`end_pw_value` specifies the ending `pw` value.

Examples: `findpw`
`findpw(start_pw_value, end_pw_value)`

Related:

`pulsecal`	Create, modify, or delete entry in pulsecal rf calibration file (P)
`pw`	Pulse width (P)
`s2pul`	Set up parameters for standard two-pulse sequence

flashc **Convert compressed 2D data to standard 2D format (C)**

Syntax: `flashc(<'nf'>,'ms'|'mi'|'rare',ns,traces,echoes)`

Description: Converts 2D FID data files from compressed formats (`seqcon='nncsn'`, `seqcon='nccnn'`, `seqcon='nnccn'`) to standard format (`seqcon='ncsnn'`) or from standard format to compressed format. Compressed data is taken by using the `nf` parameter; that is, compressed data is acquired as one large uninterrupted "multiFID" acquisition.

`flashc` reads the file `fid` in the `acqfil` subdirectory of the current experiment.

`flashc` can convert a compressed-compressed multislice, multiecho, or multi-image sequence. It can also convert a "rare" type sequence with a compressed phase-encode echo train.

`flashc` changes the values of the following VNMR parameters:

Compressed-compressed or Standard Format to Compressed Format

- `ni` is set to 1 if no argument is provided.
- `nf` is set to the value of `nf` divided by the multislice, `ms`, or multi-image, `mi`, value.
- `arraydim` is set to the product of its original value and the value of the `traces` argument.
- `arrayelemts` is set to 1 if no parameters were arrayed during data acquisition or to 2 if any parameter was arrayed during data acquisition.

Compressed Format to Standard Format

- `nf` is set to the value of the `traces` argument, or to 1 if no argument is provided.
- `ni` is set to the value of `nf` divided by the multislice, `ms`, or multi-image, `mi`, value.
- `arraydim` is set to the product of its original value and the original value of `nf`.
- `arrayelemts` is set to 1 if no parameters were arrayed during data acquisition or to 2 if any parameter was arrayed during data acquisition.

Arguments: `nf` is the number of FIDs in the second dimension of a 2D experiment. When converting data in the standard format to a compressed format, `nf` must always be the first argument.

When converting compressed-compressed or "rare" type sequences, the first argument must be a string defining the type of compression:

- `'mi'` is a keyword for the multi-image type of compression.
- `'ms'` is a keyword for the multislice type of compression.
- `'rare'` is a keyword for the "rare" multiecho, rare type, fast-imaging data sets.

(Standard to compressed) `ns` is the number of images slices or array elements to be retained.

(Compressed-compressed or rare to standard) `traces` is the number of compressed traces to retain for each `ni`. The parameter `nf` is set to this number after `flashc` has run.

(Compressed-compressed or rare to standard) `echoes` is the number of compressed echoes, used with "rare" type formatting.

Examples: **Compressed-compressed or Standard Format to Compressed Format**

`flashc('nf')` (standard to compressed)
`flashc('nf','ms',ns)` (compressed phase-encode and multi-slice)
`flashc('nf','mi',ns)` (compressed multi-image and phase-encode)

Compressed-compressed Format or Rare Format to Standard Format

`flashc` (simple compressed phase-encode)
`flashc('ms',ns)`(compressed phase-encode and multi-slice)
`flashc('mi',ns)` (compressed multi-image and phase-encode)
`flashc('rare',ns,etl)`

Related:

`arraydim`	Dimension of experiment (P)
`ft2d`	Fourier transform 2D data (C)
`ft3d`	Fourier transform 3D data (C)
`nf`	Number of FIDs (P)

`ni`	Number of increments in 1st indirectly detected dimension (P)
`seqcon`	Acquisition loop control (P)

`ft` **Fourier transform 1D data (C)**

Syntax: (1) `ft<(<options,><'nf'><,start><,finish><,step>)>`
(2) `ft('inverse',exp_number,expansion_factor)`

Description: In syntax 1, performs a Fourier transform on one or more 1D FIDs without weighting applied to the FID. `ft` executes a left-shift, zero-order phase rotation, and a frequency shift (first-order phase rotation) according to the parameters `lsfid`, `phfid`, and `lsfrq`, respectively, on the time-domain data, prior to Fourier transformation. The type of Fourier transform to be performed is determined by the parameter `proc`. Solvent suppression is turned on or off with the parameters `ssfilter` and `ssorder`. For arrayed data sets, `ft` Fourier transforms all of the array elements. To Fourier transform selected array elements, `ft` can be passed numeric arguments.

In syntax 2, `ft` performs an inverse Fourier transform of the entire spectrum. (VNMR does not currently support inverse Fourier transformation of arrayed 1D or 2D data sets.)

Arguments: `options` can be any of the following (all string arguments must precede the numeric arguments):

- `'acq'` is a keyword to check if any elements of a multi-FID experiment have already been transformed. If so, these previously transformed elements will not be retransformed.
- `'nodc'` is a keyword to not perform the usual FID drift correction.
- `'nods'` is a keyword to prevent an automatic spectral display (`ds`) from occurring. This outcome is useful for various plotting macros.
- `'noft'` is a keyword to skip the Fourier transform, thereby allowing use of all spectral manipulation and plotting commands on FIDs.
- `'zero'` is a keyword to zero the imaginary channel of the FID prior to the Fourier transform. This zeroing occurs after any FID phasing. Its use is generally limited to wideline solids applications.

`'nf'` is a keyword that makes a single FID element containing `nf` traces to be transformed as if it were `nf` separate FID elements. If `'nf'` precedes the list of numeric arguments, the rules for interpreting the numeric arguments change slightly. Passing no numeric arguments results in the transformation of all `nf` traces in the first FID element. Passing a single numeric argument results in the transformation of all `nf` traces in the requested FID element (e.g., `ft('nf',3)` transforms all `nf` traces for element 3). Regardless of the requested FID element, the resulting spectra are labeled as 1 to `nf` because multiple elements cannot be transformed using `ft('nf')`. Subsequent numeric arguments are interpreted as previously described.

`start` is the index of a particular element to be transformed. For an array, `start` is the index of the first element to be transformed.

`finish` is the index of the last element to be transformed for an array.

`step` specifies the increment between successive elements that are to be transformed for an array. The default is 1.

`'inverse'` is a keyword specifying an inverse Fourier transform.

`exp_number` is the number of the experiment, from 1 to 9, for storing the resulting FID from the inverse Fourier transform.

`expansion_factor` defines the expansion of the spectrum before the inverse Fourier transform is performed. This argument is equivalent to a multiplier for the `fn` parameter. The multiplier is restricted to between 1 and 32 and is rounded up internally to the nearest power of 2.

Examples:
```
ft
ft(1)
ft(3,7)
ft(2,10,2)
ft('nf',3)
```

Alternate: Transform button in the 1D Data Processing Menu.

Related:

`dcrmv`	Remove dc offsets from FIDs in special cases (P)
`fn`	Fourier number in directly detected dimension (P)
`lsfid`	Number of points to left-shift the `np` FID (P)
`lsfrq`	Frequency shift of the `fn` spectrum in Hz (P)
`nf`	Number of FIDs (P)
`phfid`	Zero-order phasing constant for `np` FID (P)
`proc`	Type of processing on the `np` FID (P)
`ssfilter`	Full bandwidth of digital filter to yield a filtered FID (P)
`ssorder`	Order of polynomial to fit digitally filtered FID (P)
`wft`	Weight and Fourier transform 1D data (C)

`ft2d` Fourier transform 2D data (C)

Syntax: (1) `ft2d(array_element)`

(2) `ft2d<(<options,><plane_number,><coefficients>)>`

(3) `ft2d('ni'|'ni2',element_number,increment)`

(4) `ft2d('ni'|'ni2',increment,<coefficients>)`

Description: Performs the complete 2D Fourier transformation, without weighting, in both dimensions. If the first Fourier transformation has already been done using `ft1d`, `wft1d`, `ft1da`, or `wft1da`, the `ft2d` command performs only the second (t_2) transform.

Arguments: `array_element` is a single array element to be transformed.

`options` can be any of the following (all string arguments must precede the numeric arguments):

- `'ptype'` is a keyword to transform P-type data to yield a P-type contour display.
- `'ntype'` is a keyword to transform N-type data to yield a P-type contour display. This is the default.
- `'t2dc'` is a keyword to apply a dc correction to each t_2 FID prior to the first Fourier transform. The last 1/16-th of the time domain data is used to calculate the dc level.
- `'t1dc'` is a keyword to apply a dc correction to each t_1 interferogram prior to the second Fourier transform. The last 1/16-th of the time domain data is used to calculate the dc level.
- `'f2sel'` is a keyword to allow only preselected f_2 regions to be transformed along t_1. The t_1 interferograms in the non-selected f_2

regions are zeroed but *not* transformed. The same mechanism used to select baseline regions for baseline correction (`bc`) is used to select the f_2 regions to be transformed along t_1. Set `intmod='partial'` and partition the integral of the spectrum into several regions. The even numbered f_2 regions (e.g., 2, 4, 6) are transformed along t_1; the odd numbered regions are not transformed along t_1.

- `'nf'` is a keyword to transform a non-arrayed 2D experiment that has been collected as a single 2D FID with multiple (`nf`) traces.
- `'ni2'` is a keyword to transform non-arrayed 2D data that have been collected with `ni2` and `sw2` (instead of `ni` and `sw1`). `addpar('3d')` creates the necessary processing parameters for the `'ni2'` operation.
- `'noop'` is a keyword to not perform any operation on the FID data. This option is used mainly to allow macros, such as `wft2da`, to have the same flexibility as commands.

`coefficients` are a series of coefficients according to the following scheme: `RR1` is the coefficient used to multiply the real part (first `R`) of spectra set 1 before it is added to the real part (second `R`) of the interferogram. `IR2` would thus represent the contribution from the imaginary part of spectra set 2 to the real part of the interferogram, and so forth. The scheme is depicted below.

`ft2d(RR1,IR1,RR2,IR2,...,RI1,II1,RI2,II2,...)`

where:

```
RR1*REAL(w2,element=1) ->   REAL(t1)
IR1*IMAG(w2,element=1) -> + REAL(t1)
RR2*REAL(w2,element=2) -> + REAL(t1)
IR2*IMAG(w2,element=2) -> + REAL(t1)
. . .
RI1*REAL(w2,element=1) ->   IMAG(t1)
II1*IMAG(w2,element=1) -> + IMAG(t1)
RI2*REAL(w2,element=2) -> + IMAG(t1)
II2*IMAG(w2,element=2) -> + IMAG(t1)
```

`'ni'` is a keyword to selectively transform a particular `np-ni` 2D plane within a non-arrayed 3D data set. To identify the plane, `'ni'` is followed by the `plane_number` argument, an integer from `1` through `ni2`.

`'ni2'` is a keyword to selectively transform a particular `np-ni2` 2D plane within a non-arrayed 3D data set. To identify the plane, `'ni2'` is followed by the `plane_number` argument, an integer from `1` through `ni`.

`element_number` is the number of an element within the explicit array when selectively processing an arrayed 3D data set; it ranges from `1` to `ni2`

`increment` is the increment within the explicit array when selectively processing an arrayed 3D data set; it ranges `1` to `arraydim/(ni*ni2).`

Examples:
```
ft2d(1,0,0,0,0,0,1,0)
ft2d(1)
ft2d('ptype',...)
```

Related:

`dconi`	Interactive 2D data display (C)
`dcrmv`	Remove dc offsets from FIDs in special cases (P)
`fpmult`	First point multiplier for `np` FID data (P)
`fpmult1`	First point multiplier for `ni` interferogram data (P)

ft1d	Fourier transform along f_2 dimension (C)
lsfid	Number of complex points to left-shift np FID (P)
lsfid1	Number of complex points to left-shift ni interferogram (P)
lsfid2	Number of complex points to left-shift ni2 interferogram (P)
lsfrq	Frequency shift of the fn spectrum (P)
lsfrq1	Frequency shift of the fn1 spectrum (P)
lsfrq2	Frequency shift of the fn2 spectrum (P)
parfidss	Create parameters for time-domain solvent subtraction (M)
phfid	Zero-order phasing constant for np FID (P)
phfid1	Zero-order phasing constant for ni interferogram (P)
phfid2	Zero-order phasing constant for ni2 interferogram (P)
proc	Type of processing on np FID (P)
proc1	Type of processing on ni interferogram (P)
proc2	Type of processing on ni2 interferogram (P)
pmode	Processing mode for 2D data (P)
ssorder	Order of polynomial to fit digitally filtered FID (P)
ssfilter	Full bandwidth of digital filter to yield a filtered FID (P)
wft1d	Weight and Fourier transform f_2 for 2D data (C)
wft2d	Weight and Fourier transform 2D data (C)

ftnf — Fourier-transform data acquired in compressed mode with nf (M)

Syntax: `ftnf`

Description: Fourier-transforms data acquired in compressed mode with parameter nf.

Examples: `ft('nf')` is for one-dimensional data.
`ft2d('nf')` is for two-dimensional data.

Related:

flashc	Convert compressed 2D data to standard 2D format (M)
ft	Fourier transform 1D data (C)
ft2D	Fourier transform 2D data (C)

ga — Submit experiment to acquisition and FT the result (M)

Syntax: `ga<(<'nocheck'><,'next'><,'wait'>)>`

Description: Performs experiment described by the current acquisition parameters, checking parameters loc, spin, gain, wshim, load, and method to determine the necessity to perform various actions in addition to simple data acquisition. This may involve a single FID or multiple FIDs, as in the case of arrays or 2D experiments. ga causes the data to be automatically weighted and Fourier transformed (wft) at the end of each FID data acquisition.

Before starting the experiment, ga executes two user-created macros if they exist. The first is usergo, a macro that allows the user to set up general conditions for the experiment. The second is a macro whose name is formed by go_ followed by the name of the pulse sequence (from seqfil) to be used (e.g., go_s2pul, go_dept). The second macro allows a user to set up experiment conditions suited to a particular sequence.

Arguments: 'nocheck' is a keyword to override checking if there is insufficient free disk space for the complete 1D or 2D FID data set to be acquired.

'next' is a keyword to put the experiment started with ga('next') at the head of the queue of experiments to be submitted to acquisition.

'wait' is a keyword to stop submission of experiments to acquisition until wexp processing of the experiment, started with ga('wait'), is finished.

Alternate: Go,Wft button in the Acquire Menu.

Related:

`au`	Submit experiment to acquisition and process data (M)
`change`	Submit a change sample experiment to acquisition (M)
`gain`	Receiver gain (P)
`go`	Submit experiment to acquisition (M)
`go_`	Pulse sequence setup macro called by `go`, `ga`, and `au` (M)
`load`	Load status of displayed shims (P)
`loc`	Location of sample in tray (P)
`lock`	Submit an Autolock experiment to acquisition (C)
`method`	Autoshim method (P)
`sample`	Submit change sample, Autoshim experiment to acquisition (M)
`seqfil`	Pulse sequence name (P)
`shim`	Submit an Autoshim experiment to acquisition (C)
`spin`	Submit a spin setup experiment to acquisition (C)
`spin`	Sample spin rate (P)
`su`	Submit a setup experiment to acquisition (M)
`usergo`	Experiment setup macro called by `go`, `ga`, and `au` (M)
`wft`	Weight and Fourier transform 1D data (C)
`wshim`	Conditions when shimming is performed (P)

go — Submit experiment to acquisition (M)

Syntax: `go<(<'acqi'><,'nocheck'><,'nosafe'><,'next'>`
`<,'wait'>)>`

Description: Performs the experiment described by the current acquisition parameters, checking parameters `loc`, `spin`, `gain`, `wshim`, `load`, and `method` to determine the necessity to perform various actions in addition to simple data acquisition. This may involve a single FID or multiple FIDs, as in the case of arrays or 2D experiments. `go` acquires the FID and performs no processing. If free disk space is insufficient for the complete 1D or 2D FID data set to be acquired, `go` prompts the user with an appropriate message and aborts the acquisition initiation process.

Before starting the experiment, `go` executes two user-created macros if they exist. The first is `usergo`, a macro that allows the user to set up general conditions for the experiment. The second is a macro whose name is formed by `go_` followed by the name of the pulse sequence (from `seqfil`) to be used (e.g., `go_s2pul`, `go_dept`). The second macro allows a user to set up experiment conditions suited to a particular sequence.

Arguments: `'acqi'` is a keyword to submit an experiment for display by the `acqi` program. All operations explained above are performed, except acquisition of data is not initiated. The instructions to control data acquisition are stored so that `acqi` can acquire the data when the FID button is clicked. The `gf` macro is recommended instead of running `go('acqi')` directly. Using `gf` prevents certain acquisition events from occurring, such as spin control and temperature change. See the description of `gf` for more information.

`'nocheck'` is a keyword to override checking if there is not enough free disk space for the complete 1D or 2D FID data set to be acquired.

`'nosafe'` is a keyword to disable probe protection during the experiment.

`'next'` is a keyword to put the experiment started with `go('next')` at the head of the queue of experiments to be submitted to acquisition.

`'wait'` is a keyword to stop submission of experiments to acquisition until `wexp` processing of the experiment, started with `go('wait')`, is finished.

Examples: `go`
`go('nosafe')`

Alternate: Go button in the Acquire Menu."

Related:

`acqi`	Interactive acquisition display process (C)
`au`	Submit experiment to acquisition and process data
`change`	Submit a change sample experiment to acquisition (M)
`gain`	Receiver gain (P)
`ga`	Submit experiment to acquisition and FT the result (C)
`gf`	Prepare parameters for FID/spectrum display in acqi (M)
`go_`	Pulse sequence setup macro called by `go`, `ga`, and `au` (M)
`load`	Load status of displayed shims (P)
`loc`	Location of sample in tray (P)
`lock`	Submit an Autolock experiment to acquisition (C)
`method`	Autoshim method (P)
`probe_protection`	Probe protection control (P)
`sample`	Submit change sample, Autoshim exp. to acquisition (M)
`seqfil`	Pulse sequence name (P)
`shim`	Submit an Autoshim experiment to acquisition (C)
`spin`	Submit a spin setup experiment to acquisition (C)
`spin`	Sample spin rate (P)
`su`	Submit a setup experiment to acquisition (M)
`usergo`	Experiment setup macro called by `go`, `ga`, and `au` (M)
`wshim`	Conditions when shimming is performed (P)

`image` Display noninteractive gray scale image (M)

Applicability: Systems with imaging capabilities.

Syntax: `image`

Description: Brings up a `dcon` 2D display of an image (using grayscale and linear scaling of the intensity) that can be used for adjusting the display while using `dconi`.

Related:

`dcon`	Display noninteractive color intensity map (C)
`dconi`	Interactive 2D data display (C)
`dconn`	Display color intensity map without erasing screen (C)

`imageprint` Print currently displayed image on plotter (C)

Syntax: `imageprint`

Description: Produces a dithered density map of the currently displayed image and sends it to the current plot device. The dithered image prints in reverse contrast (black for white) so that the gray tones are inverted in the plot output. `imageprint` is not suitable for pen plotters.

Alternate: Image button on the 2D Plotting Menu.

See also: *User Guide: Liquids*

Related:

`plot`	Automatically plot spectra (M)

`imark` Label a 2D image or spectrum (M)

Syntax: `mark(label<,color>)`

Description: Writes a label to a point on an interactive 2D image or spectrum determined by the intersection of the cursors.

Arguments: `label` is a string argument for the label.

`color` specifies the color of the label.

Examples: `imark('Spectrum 1')`
`imark('Spectrum 1','yellow')`.

Related: `write` Write formatted text to a device (C)

`imcalc` **Arithmetic & other manipulations on 2D images/phasefiles (M, UNIX)**

Syntax: (From VNMR) `imcalc(optype,phf1,<phf2,outphf,args)>`

(From UNIX) `imcalc optype phf1 <phf2 outphf args>`

Description: Performs arithmetic and spatial manipulations on 2D images on a pixel-by-pixel basis. The operands used by `imcalc` are phasefiles that must have been previously saved with the VNMR command `svphf`.

`imcalc` can be accessed with the `imcalci` macro or in one of the following three modes:

- Direct execution of the UNIX program from a UNIX shell (not recommended)
- Executed from VNMR with the appropriate arguments (recommended only for macro-controlled repetitive operations)
- Executed from VNMR with no arguments (recommended mode)

Limitation on `imcalc`:

The `trace` parameter must be set to `'f1'` when saving phasefiles for use with `imcalc`, and when displaying phasefiles resulting from calculations.

Trying to display an absolute value phasefile in an experiment in which `'ph'` mode is selected (or vice-versa) does not work. See the following subsection, "Helpful Hints," for a solution to this problem.

If a nonsquare image is rotated 90 degrees, the result is not displayed with the correct aspect ratio, because the `lro` and `lpe` parameters are not altered by this procedure.

The same phasefile cannot be used for both operands in a binary operation. To do this, make a copy of the desired phasefile and give it a different name

Arguments: Entering `imcalc` with no arguments displays a menu system that allows the following selection of a number of different 2D image mathematical or spatial manipulations. Selection of the desired image operation menu button results in prompts to the user for required input information, such as the name of a phasefile or a numerical constant. Unary operations, such as square root or log, do not require user input and are immediately executed when selected by using the phasefile resident in the current experiment.

`optype` can be any of the following keywords (place single quotes around the keyword when entering `imcalc` from VNMR).

`add`	Add two images.
`sub`	Subtract second image from first (from UNIX, use `add` with a negative multiplier).
`mult`	Multiply two images.
`div`	Divide first image the second, with noise thresholding.

`add`	Add two images.
`vadd`	Add two orthogonal images to form vector sum (result = sqrt [image1**2 + image2**2]).
`phase`	Compute phase angle determined by arctan of two images.
`mean`	Arithmetic mean of two images (result = [image1 + image2]/2).
`gmean`	Geometric mean of two images (result = sqrt[image1*image2]).
`addc`	Add a constant value to each pixel in an image.
`multc`	Multiply each pixel in an image by a constant value.
`abs`	Absolute value.
`log`	Logarithm (result = log10[abs(image)]).
`exp`	Antilog (result = 10**image).
`pow`	Exponentiation (result = image**constant).
`reverse`	Linear inversion of pixel intensities (reverse contrast).
`clipmax`	Set pixel values above a user-supplied maximum to zero.
`clipmin`	Set pixel values below a user-supplied minimum to zero.
`thresh`	Compress pixel values above a selected threshold `thresh` to 1, and below a threshold to 0.
`thresh2`	Compress all pixel values above a user-supplied minimum and below a user-supplied maximum to 1, all others to 0.
`f1roll`	Wrap image in F1 direction a selected number of pixels.
`f2roll`	Wrap image in F2 direction a selected number of pixels.
`flip_horiz`	Flip image about central horizontal axis.
`flip_vert`	Flip image about central vertical axis.
`flip_diag`	Flip image about *x*=*y* diagonal (only square images).
`rotate_90`	Rotate image clockwise 90 degrees (only square images).
`rotate_180`	Rotate image 180 degrees.
`vline`	Replace a selected vertical trace by average of two adjacent traces.
`hline`	Replace a selected horizontal trace by average of two adjacent traces.

Examples: (From UNIX) `imcalc add phf1 phf2 outphf 0.5`
(From VNMR) `imcalc('add','phf1','phf2')`

Related:

`imcalc`	Interactive prompt for imcalc (M)
`rtphf`	Return a stored phasefile into the current VNMR experiment (M)
`svphf`	Save currently displayed phasefile to planes directory (M)

`imcalci` Interactive prompt for imcalc (M)

Syntax: `imcalci(optype)`

Description: Serves as an interactive interface to the `imcalc` macro by prompting for any required inputs, which vary with operation type. `imcalci` can be run from the VNMR command line, or accessed via the `imcalc` menu system by selecting

the ImageCalc option in the Analyze menu, or by entering the command `imcalc` with no arguments.

Arguments: `optype` has the same values as described for the `imcalc` macro.

Examples: `imcalc('add')`

Related: `imcalc` Interactive prompt for imcalc (M)

`imconi` **Display 2D data in interactive grayscale mode (M)**

Syntax: `imconi`

Description: Calls the `dconi` program with the arguments required for grayscale image display: `dconi('dcon','gray','linear')`.

Related: `dconi` Interactive 2D contour display (C)

`imconn` **Display 2D data without erasing the screen (M)**

Syntax: `imconn<(file)>`

Description: Displays a noninteractive grayscale 2D image without erasing the screen before drawing. `imconn` can be used to display two or more images on the screen simultaneously, from the same or different experiments.

For example, to display two image phasefiles in a single experiment, first adjust the chart size and position and display the first image, then adjust chart position and retrieve the second image with `imconn('name2')`, where `name2` is the name of the second phasefile.

Images in two different experiments can be simultaneously displayed by using `jexp` with the desired experiment number as an argument: in the first experiment, adjust the display parameters, for example, left to display the image on the left side of the screen, then use `jexp(6)` to join experiment 6 without erasing the screen, followed by right and `imconn` to position and display the image in second experiment on the right side of the screen without erasing the first image.

Arguments: `file` is the image phasefile name.

Examples:
`imconn`
`imconn('image1')`

Related:

`dconi`	Interactive 2D contour display (C)
`dmi`	Transform and display multiple images in graphics window (M)
`jexp`	Join existing experiment (C)
`rtphf`	Return a stored phasefile into the current VNMR experiment (M)
`imconi`	Display 2D data in interactive grayscale mode (M)
`svphf`	Save currently displayed phasefile to planes directory (M)

`imfit` **Process arrayed 2D imaging data and fit to T1 or T2 map (M, UNIX)**

Syntax: (From VNMR)`imfit('t1'|'t2',basename,min_threshold)`

(From UNIX) `imfit t1|t2 basename min_threshold time1 time2...timeN`

Description: Fits an arrayed set of 2D image data and computes a pixel-by-pixel T_1 or T_2 map. The `imfit` macro provides a convenient link to the fitting program by automatically constructing and passing the required arguments to the UNIX

`imfit` program. The `imfit` macro requires the following information as arguments that it passes to the UNIX program:

- A fitting type - either T_1 for inversion-recovery or T_2 for decaying exponential.
- A base name for the collection of phasefiles that represents the arrayed set of images. These phasefiles must reside in the planes directory of the current experiment, and must end in consecutive integer extensions starting with 1.
- A noise threshold value specifying the lower limit for the fitting program.

Pixels whose values in the first image are less than this threshold are not fit, and are assigned values of zero in the computed T_1 or T_2 image.

Three computed images are constructed by the `imfit` program, and placed in the planes directory of the current experiment. The T_1 or T_2 image is named `basenamet1` or `basenamet2`. An error image (`basenamesigma`) represents the standard deviation of the fit at each pixel, and `basenamem0` (the `t=0` default) represents the intercept of the original data at time zero. Pixels in the T_1 or T_2 map that cannot be reliably fitted are set to zero.

The `imfit` macro automatically extracts the timing values for each array element in the data set from the parameter that it finds arrayed, and passes the list of values to the `imfit` fitting program. Only a single arrayed parameter is supported. If the data cannot be handled by the `imfit` macro, it is possible to call the external `imfit` program directly as you would any other UNIX program. The command line arguments must be constructed manually in this case. The syntax required for a direct UNIX `imfit` call is:

```
imfit t1|t2 basename minthresh time1 time2....timeN
```

As an example, with a set of phasefiles representing T_1 data, and named `phantom1, phantom2,...`, use:

```
imfit('t1','phantom',threshold)
```

To obtain a value for the noise threshold, display an image, place a cursor box over a region of noise, and select the Mark button. Divide the displayed value of “height” by vs and use the result as the threshold. The macro `makephf` can be used to transform all of the images and save them as phasefiles. `t1image` automatically does this entire procedure, prompting you for the required information.

Note that an error in `imfit` is that a T_1 fitting type requires phase-sensitive images progressing from negative to positive in the normal inversion-recovery model.

Arguments: `'t1'` and `'t2'` are keywords for the fitting type, either `'t1'` for inversion-recovery or `'t2'` for decaying exponential (`'t2'` can also be used for saturation-recovery data).

`basename` is the name of a phasefile that represents the arrayed set of images. The phasefile should reside in the `planes` directory and must end in consecutive integer extensions, starting with `1`.

`min_threshold` is a value for the lower limit for the fitting program. Pixels whose values in the first image are less than this threshold will not be fit and will be assigned values of zero in the synthesized resultant images.

Related:

Related:	`expfit`	Make least-squares fit to polynomial or exponential curve (U)
	`makephf`	Transform arrayed imaging data and save as phasefiles (M)
	`t1image`	Compute a pixel-by-pixel T_1 map (M)

`lleft` Set chart parameters to display 2D data in lower-left corner (M)

Syntax: `lleft`

Description: Computes the chart position and size parameters `sc`, `sc2`, `wc`, and `wc2` to place the 2D display area in the lower-left quadrant of the VNMR graphics screen.

Related:

`lright`	Set chart parameters to display 2D data in lower right corner (M)
`uleft`	Set chart parameters to display 2D data in upper left corner (M)
`uright`	Set chart parameters to display 2D data in upper right corner (M)

`lright` Set chart parameters to display 2D data in lower right corner (M)

Syntax: `lright`

Description: Computes the chart position and size parameters `sc`, `sc2`, `wc`, and `wc2` to place the 2D display area in the lower right quadrant of the VNMR graphics screen.

Related:

`lleft`	Set chart parameters to display 2D data in lower left corner (M)
`uleft`	Set chart parameters to display 2D data in upper left corner (M)
`uright`	Set chart parameters to display 2D data in upper right corner (M)

`makephf` Transform arrayed imaging data and save as phasefiles (M)

Syntax: `makephf(basefile<,upper_limit>)`

Description: Performs a 2D Fourier transform on each element of an arrayed imaging data set and saves the resulting images as sequentially numbered phasefiles.

Arguments: `basefile` is a phasefile name. An incremented numerical extension, starting with 1, is added to this basename to form a set of numbered phasefiles in the planes directory of the current experiment.

`upper_limit` specifies an upper limit to the number of arrayed elements to be processed. The default is that all images are transformed and saved.

Examples:
```
makephf('phantom')
makephf('fleming',10)
```

Related:

`svphf`	Save currently displayed phasefile to planes directory (M)

`markvs` Display data value at cursor position in a 2D display (M)

Syntax: `markvs`

Description: Displays the data value at the cursor position in a 2D display.

`markvs` runs the VNMR `mark` command, divides the obtained height by the vertical scale parameter, `vs`, and displays the resulting true data value.`mark` displays the "height" of the data at the point designated by the intersection of the two cursors in a 2D display. In actuality, this "height" is the true data value multiplied by `vs`.

For example, it is useful to know the true data value to determine the T_1 value from a T_1 map computed by `imfit`, or the phase angle in a phase map image.

Related:

`imfit`	Process arrayed 2D imaging data and fit to T_1 or T_2 map (M)
`mark`	Determine intensity of spectrum at a point (C)
`vs`	Vertical scale (P)

`math` Execute expr (C)

Syntax: `math('expr')`

Description: Executes the expression `expr` in the same way as if it had been typed into the Image Math panel.

pcmapapply **Apply Phase Correction Map to Data (C)**

Applicability: Systems with echo planar imaging capabilities.

Syntax: `pcmapapply ([<file>,]<index>)`

Description: Applies a pixel-by-pixel phase shift to the current data file using the complex phase correction values from the phase correction map file `$vnmruser/expN/datdir/<file>`. `file` must reside in your `$vnmruser/expN/datdir` directory where `N` is the current experiment number.

Phase correction values are generated by `pcmapgen`.

`pcmapapply` opens and closes a phase map file unless it has been explicitly opened with `pcmapopen`.

Arguments: `file` specifies the phase correction map file name that resides in your `$vnmruser/expN/datdir` directory. The default file is `$vnmruser/expN/datdir/pcmap`. If you do not provide `file`, `pcmapapply` defaults to the `pcmap` file.

`index` specifies which phase correction map to us in the file. This value will usually be 1. This argument, which must always be supplied, ranges from 1 to n; it specifies the desired correction map block within the file.

Examples: `pcmapapply(1)`

Related:

pcmapclose	Close phase correction map file (C)
pcmapgen	Generate phase correction map (C)
pcmapopen	Open phase correction map file (C)

pcmapclose **Close Phase Correction Map (C)**

Applicability: Systems with echo planar imaging capabilities.

Syntax: `pcmapclose`

Description: Closes a phase correction map file that was explicitly opened with the `pcmapopen` command.

Examples: `pcmapclose`

Related:

pcmapapply	Apply phase correction map to data (C)
pcmapgen	Generate phase correction map (C)
pcmapopen	Open phase correction map file (C)

pcmapgen **Generate Phase Correction Map (C)**

Applicability: Systems with echo planar imaging capabilities.

Syntax: `pcmapgen ([<file>,]<index>)`

Description: Generates pixel-by-pixel complex phase correction values from the current data file and stores them into the `<index>` block in the phase correction map file `$vnmruser/expN/datdir/<file>`. `file` must reside in your `$vnmruser/expN/datdir` directory where `N` is the current experiment number.

One or more phase correction maps can be generated. In the case of a multislice echo planar imaging experiment, there can be one phase correction map for each slice.

`pcmapgen` creates, opens, and closes a phase map file unless the file has been explicitly opened with the `pcmapopen` command.

Arguments: `file` specifies the phase correction map file name residing in your `$vnmruser/expN/datdir` directory. The default file is `$vnmruser/expN/datdir/pcmap`. If you do not provide `file`, `pcmapgen` defaults to the file name `pcmap`.

You must always provide `index`, which ranges from 1 to n (this value is usually 1), and specifies the desired correction map block within the file.

Examples: `pcmapgen(1)`

Related:

pcmapapply	Apply phase correction map to data (C)
pcmapclose	Close phase correction map file (C)
pcmapopen	Open phase correction map file (C)

pcmapopen — Open Phase Correction Map (C)

Applicability: Systems with echo planar imaging capabilities.

Syntax: `pcmapopen ([<file>,]<max_index>)`

Description: Explicitly opens a phase correction map file, which can significantly speed up data processing. `file` must reside in your `$vnmruser/expN/datdir` directory where `N` is the current experiment number. After the map file is open, use `pcmapgen` and `pcmapapply` to generate maps and correct data. Use `pcmapclose` to close the file when you are finished with it.

Arguments: `file` specifies the phase correction map file name residing in your `$vnmruser/expN/datdir` directory. Without this argument, `pcmapopen` defaults to `pcmap`.

`max_index` specifies the maximum number of phase correction maps in the file, and ensures memory mapping extends to or past the end of the file. You must always provide `max_index`, which must be greater than or equal to the maximum number of phase maps stored in the file.

Examples: `pcmapopen('pcmap',2)`

Related:

pcmapapply	Apply phase correction map to data (C)
pcmapclose	Close phase correction map file (C)
pcmapgen	Generate phase correction map (C)

rtphf — Return a stored phasefile into the current VNMR experiment (C)

Syntax: `rtphf(phasefile)`

Description: Copies a stored phasefile from the `planes` directory in the current experiment directory to the working phasefile file in the `datdir` directory of the current experiment.

Copying a stored phasefile allows the display and manipulation of previously transformed images, or results of image calculations from `imcalc` or `imfit`. It also allows the display of multiple images in VNMR (see `imconn`).

`rtphf` is commonly used to load stored phasefiles that have been processed and saved in a single experiment from a single data set, for example, a multislice imaging experiment. However, any phasefile from any experiment or image processing routine can be retrieved using `rtphf` if it has the right pixel dimensions and header information. The phase file must first be copied into the local experiment `planes` directory. `rtphf` matches the pixel matrix

dimensions and header information against the processed data file, and if there are differences, `rtphf` fails. For example, any phasefile stored in phase-sensitive mode cannot be successfully loaded into an experiment where the data has been processed in absolute value mode, because the headers for absolute value and phase-sensitive phasefiles differ (see `imcalc` for hints).

Regarding errors, an `rtphf` failure is not catastrophic; that is, it will not crash VNMR and will not harm the resident raw or processed data in any way. But, it will result in display of the previous phasefile found in `datdir`.

Arguments: `phasefile` is the name of a stored phase file. This file must have been saved previously with `svphf` or by some other process, such as `imcalc`, `imfit`, or a user-written program. The named phasefile should be in the `planes` directory in the current experiment (e.g., `vnmrsys/exp4/planes`).

`Examples:` `rtphf('fleming')`

Related:		
	`imcalc`	Interactive prompt for imcalc (M
	`imconn`	Display 2D data without erasing the screen (M)
	`svphf`	Save currently displayed phasefile to planes directory (M)

`setgn` Automatically set receiver gain (M)

Syntax: `setgn`

Description: Automatically determines the receiver gain, based on the input signal.

Related:		
	`gain`	Receiver gain (P)

`spuls` Load default single pulse sequence imaging parameters (M)

Syntax: `spuls`

Description: Loads `s2pul` pulse sequence parameters. The parameters are initialized for imaging experiments. For example, parameters such as `lock`, `spin`, and `temp` are initialized to `'n'`.

Related:		
	`s2pul`	Set up parameters for standard two-pulse sequence

`ssprep` Calculate slice gradient and slice selection parameters (M)

Applicability: Systems with echo planar imaging (EPI) capabilities.

Syntax: `ssprep`

Description: Calculates the slice gradient parameter, `gss`, and the slice selection parameters, `tpwr1` and `tpwr2`, for use in the EPI experiment. Unlike `imprep`, readout and phase encode related parameters are not modified by `ssprep`.

Related:		
	`gss`	Slice selection gradient strength (P)
	`imprep`	Calculate gradient and rf parameters for imaging (M)
	`tpwr1`	Intensity of an excitation pulse (P)
	`tpwr2`	Intensity of an inversion pulse (P)

`stats` Calculate statistics of points specified by cursor position (M)

Syntax: `stats`

Description: Computes the mean, range, and standard deviation of the set of points defined by the cursor position in a set of arrayed 1D spectra. This function is useful in measuring the stability or reproducibility of data acquisition.

svdat **Save data (C)**

Syntax: `svdat(file<,'f'|'m'|'i'|'b'>)`

Outputs current data from the current experiment to a file. Integer data is scaled when it is written (note that `svdat` replaces the former command `svsdfd`).

Floating point data is not scaled when written but integer data is scaled when written. A data value *x* is scaled as a*x*+b where:

```
a=(vs*grays1*numgray)/64.0
b=numgray*(0.5-(grays1*grayctr/64.0))
```

where the parameter `numgray` has a default of 4096 for `'m'` and `'i'` formats and a default of 256 for the `'b'` format, `graysl` has a default of 1, and `grayctr` has a default of 32.0.

To scale 16-bit integer data other than 12-bits, the global parameter `numgray` can be created using `create(numgray,real,global)` and set to the value 2^n, where n is the number of bits desired. For example, to scale to 15-bits, set `numgray=32768`.

The display parameters `graysl` and `grayctr` are used by the macros `svib` and `svsis` to save data files for Image Browser.

Arguments: `file` is the name of the data file. The file is created in the current VNMR directory unless a full directory path is given. If a file of the same name already exists, the user is queried to overwrite the file. If a fully qualified file name is not given, the file is created in VNMR's current directory.

`'f'` is a keyword to write data in 32-bit floating point. This is the default.

`'m'` or `'i'` is a keyword to write data as 16-bit integers scaled to 12 bits.

`'b'` is a keyword to write data as 8-bit byte integers.

Examples:

```
svdat('data45')
svdat('rodent','b')
```

Related:

`browser`	Start Image Browser (U)
`fdfgluer`	Make FDF file from header and data parts (C)
`grayctr`	Gray level window adjustment (P)
`graysl`	Gray level slope (contrast) adjustment (P)
`svib`	Generate and save images as Image Browser-compatible FDF files (M)
`svsis`	Generate and save images as FDF files (M)

svf **Save FIDs in current experiment (M)**

Syntax: `svf<(file<,'nolog'><,'arch'>)>`

Description: Saves parameters, text, and FID data in the current experiment to a file. No data is removed from the current experiment; `svf` merely saves a copy of the data in a different file. You can enter `rt` to retrieve the complete data set, or enter `rtp` to retrieve parameters only.

Arguments: `file` is the name of the file, with the suffix `.fid` added, to be created to save the data. The default is the system prompts for a file name. You are warned if you attempt to overwrite a file that already exists. In fact, if data has been acquired with the `file` parameter set, the data does not need to be saved. It is already stored in a named file.

`'nolog'` is a keyword to not save the log file with the data. The default is to save the log file.

'arch' is a keyword to assume that the data goes to a database and appends to the (or creates a) doneQ file with information that can be used by the command status.

Examples: svf
svf('/home/vnmr1/mydatafile')

Related:

file	File name (P)
rt	Retrieve FID (M)
rtp	Retrieve parameters (M)
status	Display status of all experiments (C)

svib — Generate and save images as Image Browser-compatible FDF files (M)

Syntax: svib(directory<,'f'|'m'>)

Description: Generates images from the current experiment and saves them into the specified directory as Flexible Data Format (FDF) files, suitable for display in the Image Browser image processing program. svib saves a single image, or a number of images from a multislice, multiecho, or arrayed imaging experiment. The VNMR command svdat is used to write the binary image file.

Arguments: directory specifies the name of the directory to save the FDF files. svib creates the directory in the current working VNMR directory, and appends it with the extension .dat. FDF image files are created in this directory as image0001.fdf, image0002.fdf, etc. A copy of the procpar file from the current experiment is also saved in this directory.

'f' is a keyword to save the output data in 32-bit floating point format. This is the default.

'm' is a keyword to save the output data scaled to 12-bit integer and saved as 16-bit words (historical Siemens Magnetom data format).

Examples: svib('phantom')
svib('rodent.images','m')

Related:

makephf	Transform arrayed imaging data and save as phasefiles (M)
svdat	Save data (C)
svphf	Save currently displayed phasefile to planes directory (M)

svp — Save parameters from current experiment (M)

Syntax: svp(file)

Description: Saves parameters from current experiment to a file. The parameter set can be retrieved with the rtp and rt macros. svp reflects any changes made in parameters up to the moment of entering svp, including acquisition parameters (unlike macro svf).

Arguments: file is the name of the file, with the suffix .par added, to be created to save the parameters. The default is the system prompts for a file name. You are warned if you attempt to overwrite a parameter set that already exists.

Examples: svp('/vnmr/stdpar/P31')
svp('/usr/george/testdata')

Related:

rt	Retrieve FID (M)
rtp	Retrieve parameters (M)
svf	Save FIDs in current experiment (M)

svphf **Save currently displayed phasefile to planes directory (M)**

Syntax: `svphf(file)`

Description: Saves the currently displayed phasefile to a directory named `planes` in the current VNMR experiment directory. If `planes` does not already exist, `svphf` automatically creates it. `svphf` can be used to save phasefiles in absolute-value or phase-sensitive modes.

The current phasefile, found in the `datdir` directory of the current experiment, might be the result of Fourier transformation of experimental data or might be a phasefile previously loaded with the `rtphf` command. A phasefile is normally the result of apodization, Fourier transformation, and phasing or magnitude calculation, but before contrast windowing and leveling controlled by the `grayctr` and `graysl` parameters. The phasefile is a binary data file, and no parameters are stored with the phasefile.

Arguments: `file` specifies the name to be used for the stored file.

Examples: `svphf('fleming')`

Related: `rtph` Return a stored phasefile into the current VNMR experiment (M)
`svib` Generate and save images as Image Browser-compatible FDF files (M)

t1image **Compute a pixel-by-pixel T_1 map (M)**

Syntax: `t1image`

Description: Computes a pixel-by-pixel T_1 map from arrayed inversion-recovery imaging data. `t1image` performs all of the pre-processing required for fitting inversion-recovery T_1 data. It prompts for the base phasefile name and lower limit noise threshold, transforms and saves all of the images, and calls `imfit` to complete the fitting process and display the computed T_1 map. The values at each pixel in the T_1 map represent the computed T_1 in seconds.

Related: `imfit` Process arrayed 2D imaging data and fit to T_1 or T_2 map (M)

tabc **Convert data in table order to linear order (M)**

Syntax: `tabc<(dimension)>`

Description: Converts arbitrarily ordered data obtained under control of an external AP table to linear monotonic order, suitable for processing in VNMR. The data must have been acquired according to a table in the `tablib` directory.

Imaging and other 2D experiments are normally acquired so that the order of the incremented acquisition parameter, such as the phase-encode gradient, is linear and monotonic. For a standard imaging experiment, this linear order means that the phase-encode gradient progresses from a starting negative value monotonically up through zero to a positive value (e.g., –64, –63, –62, ... , –1, 0, 1, ... , 62, 63). The `ft2d` program assumes this structure in its operation.

Data from table-driven 2D pulse sequences is used by entering `tabc` *only once* before normal 2D processing and/or parameter storage. `tabc` takes no arguments and is executed by entering `tabc` in the VNMR command window. A simple check is done by `tabc` to prevent it from being executed more than once on the same data set.

`tabc` expects to find 2D data in the standard VNMR format (i.e., using the `ni` parameter); see the third example. You must specify the compressed form of data (i.e., use the `nf` parameter) and enter a value of 1 in the `dimension` argument; see the second example.

`tabc(3)` reorders 3D data acquired with an external table. 3D data is expected to be in the "compressed/standard" format, in which there are `ni` standard 2D planes of data (the third dimension), each consisting of `nf` compressed FIDs (the second dimension); see the fourth example.

`tabc` reads the file `fid` in the `acqfil` subdirectory of the current experiment. Before the data is reordered, this file is written to another file named `fid.orig` in the same `acqfil` directory. If for any reason `tabc` fails or results in an unpredictable or undesired transformation, you can salvage the original raw data by moving `fid.orig` back to `fid`. To gain more disk space, explicitly delete `fid.orig` after you are satisfied that conversion is successful.

Use `tabc` on either saved data that has been loaded into a VNMR experiment or on data in an experiment that has just been acquired but not yet saved. In the first case, converted data must be saved again for the saved data set to reflect conversion.

`tabc` supports all 2D data types recognized by VNMR: arrayed, compressed multislice, and arrayed compressed multislice.

`tabc` requires that data must have the same number of "traces" as the table elements. It does not support any of the advanced features of table expansion (e.g., the entire table must be explicitly listed in the table file), and expects to find only one table in a file; whether the table is t1 or t60 is unimportant.

Arguments: `dimension` specifies the type of data, which has been acquired with an external table, to be converted. The default is standard 2D data.

Examples: `tabc`
`tabc(1)` converts the order of compressed 2D data; `nf` specifies the second dimension.
`tabc(2)` converts the order of standard 2D data; `ni` specifies the second dimension.
`tabc(3)` converts the order of imaging 3D data; `nf` specifies the second dimension and `ni` specifies the third dimension.

Related:

`flashc`	Convert compressed 2D data to standard 2D format (C)
`ft2d`	Fourier transform 2D data (C)
`nf`	Number of FIDs (P)
`ni`	Number of increments in 1st indirectly detected dimension (P)

`tcapply` Apply table conversion reformatting to data (C)

Syntax: `tcapply<(file)>`

Description: Rearranges the spectra in a 2D data set that resides in the current data file. You must apply `ft1d` to the data before you can use this command.

Using values from an AP table, `tcapply` arranges the spectra corresponding to the value in the AP table from low value to high value. The values might have already been read in by the `tcopen` command. If you provide `file`, the values are read in from `$vnmruser/tablib/<file>`.

As an example, for a standard imaging experiment, phase encode gradients monotonically progress from a starting negative value up through zero to a positive value:

```
-64,-63,-62,...,-1,0,1,...,62,63
```

It is possible to acquire the equivalent data in nonmonotonic order, either by explicitly coding the desired progression into a pulse sequence or by using an

external AP table to control the order. In either method, `ft2d` is not able to properly process the resulting data until `tcapply` and `tabc` are applied to the data. `tcapply` and `tabc` are functions that reconstruct a properly ordered data set from any arbitrarily ordered data that has been acquired under the control of an external AP table. The data must have been acquired according to a table in the `tablib` directory. The difference between `tcapply` and `tabc` is that `tcapply` works on the first dimension transformed spectra residing in the VNMR data memory and `tabc` works on and changes the raw data in a FID file.

Arguments: `file` is an optional argument specifying the AP table to be read; the table must be in `$vnmruser/tablib/<file>`.

Examples:
```
ft1d(2)
tcapply(petable)
ft2d(2)
```

Related:

`tabc`	Convert data in table order to linear order (C)
`ft1d`	Fourier transform along f_2 dimension (C)
`ft2d`	Fourier transform 2D data (C)
`tcclose`	Close table conversion file (C)
`tcopen`	Open table convert file (C)

`tcclose` Close table conversion file (C)

Syntax: `tcclose`

Description: Removes a table conversion file and frees the memory used to store the sorted table indices read in with the `tcopen` command.

Examples: `tcclose`

Related:

`tcapply`	Apply table conversion reformatting to data (C)
`tcopen`	Open table convert file (C)

`tcopen` Open table conversion file (C)

Syntax: `tcopen<(file)>`

Description: Explicitly reads, sorts, and stores, in memory, a table conversion file in `$vnmruser/tablib/<file>`, `tcopen` uses the file when `tcapply` is called.

Arguments: `file` specifies the file to be read; it must be in `$vnmruser/tablib/<file>`.

Examples: `tcopen (petable)`

Related:

`tcapply`	Apply table conversion reformatting to data (C)
`tcclose`	Close table convert file (C)

`title` Write a title to the plotter (M)

Syntax: `title(string)`

Description: Writes a title to the plotter in the upper-left corner of the page.

Arguments: `string` is a string containing the title.

Examples: `title('June 17, 1H STEAM with 25-mm surface coil')`.

Related:

`write`	Write formatted text to a device (C)

uleft **Set chart parameters to display 2D data in upper-left corner (M)**

Syntax: uleft

Description: Computes the chart position and size parameters sc, sc2, wc, and wc2 to place the 2D display area in the upper-left quadrant of the VNMR graphics screen.

Related:

lleft	Set chart parameters to display 2D data in lower left corner (M)
lright	Set chart parameters to display 2D data in lower right corner (M)
title	Write a title to the plotter (M)
uright	Set chart parameters to display 2D data in upper right corner (M)

uright **Set chart parameters to display 2D data in upper-right corner (M)**

Syntax: uright

Description: Computes the chart position and size parameters sc, sc2, wc, and wc2 to place the 2D display area in the upper-right quadrant of the VNMR graphics screen.

Related:

lleft	Set chart parameters to display 2D data in lower left corner (M)
lright	Set chart parameters to display 2D data in lower right corner (M)
title	Write a title to the plotter (M)

A.5 Parameters

This section provides a targeted overview of the specialized parameters used in imaging and localized spectroscopy applications. The information here is a supplement to the more comprehensive manual *VNMR Command and Parameter Reference*. Additional descriptions for some parameters that are commonly used in liquids and solids NMR application, such as pw and tpwr, can be found in that manual.

Predefined Parameter Names

A large number of parameters useful for imaging and localized spectroscopy have been included in each imaging parameter set and predefined for use in pulse sequence programming. Any imaging parameter set will contain all of the parameters described in this section, so there is no need to create them. Similarly, all of these parameters are declared as variables in the file standard.h for use in pulse sequence programming, and are automatically retrieved from the parameter set.

Some parameter names are used throughout VNMR to provide automated setup of imaging experiments, such as gro and gss. New sequence applications using other parameter names can be written. However, in certain cases, automated setup features do not function as desired if alternate names are used. The list of specialized imaging parameters that VNMR expects to find includes gcoil, gmax, gro, gss, pro, pss, rfcoil, and thk. Further descriptions of these and all other predefined parameters are found in this section.

While a large number of parameters have been predefined for ease of use in pulse sequence programming, it is unlikely that any imaging sequence will use every parameter name. Instead, some subset of the entire group will be found in any given sequence. Many of the parameter names have been chosen in an attempt to provide an intuitive correspondence to the imaging literature. There is no special significance, however, to names such as gflow or gspoil. These names that have been chosen for their obvious descriptive nature, but may be used arbitrarily in a pulse sequence as desired by the user. Varian's standard imaging sequences use these names in an attempt to convey the most obvious connection to events and processes that an experienced imaging spectroscopist would recognize. In all cases,

please consult individual pulse sequence programs and manual pages for a detailed description of parameter use in that sequence.

Displaying Additional Parameter Groups Using dgm

The primary parameters of any imaging experiment can be displayed in the text window with the `dg` command, the same as for any VNMR parameter set. Most secondary parameter groups, such as `dg1` and `dgs` will be found in each imaging experiment, along with several other specialized parameter groups. These additional parameter groups allow the display, for example, of all predefined gradient parameters or all predefined rf pulse parameters, etc., although some of the displayed parameters will be unused in any given experiment and have values set to zero or to a null string.

The `dgm` command allows menu selection of the various `dg` screens in any experiment by searching for all parameter names that begin with the two letters `dg`, and presents a menu of all such names. To display any of these parameter groups, select the button with the desired description. Once a parameter group is displayed, use the Print button to print it.

Gradient Parameters

A predefined group of gradient parameters is present in all imaging parameter sets, covering the range of most imaging applications. All of these gradient parameters have units of gauss/cm, and are created in VNMR as type "real." Because the maximum gradient strength is dependent on the gradient hardware in use, there is no automatic over-range checking of gradient parameters. While a value larger than the maximum possible gradient may be assigned to a parameter, there is no risk of physical damage to the gradients because the pulse sequence functions that control gradients do check for values exceeding the allowed physical maximum.

Gradient Calibration Parameters

B0 **Magnet main static field**

Description: Field strength of the main magnetic field. This value is used by planning setup macros in their calculations.

Values: Number, in units of gauss. Nominal value is `234.9*h1freq`. For example, a 4.7T (200 MHz) system has a value of approximately 47,000.

Related: `h1freq` Proton frequency of spectrometer (P)

boresize **Magnet bore size**

Description: The internal usable diameter of the gradient set.

This parameter is used by various pulse sequence setup macros to determine the validity of the field of view and slice offset input. It is defined in the system gradient table files found in `$vnmrsystem/imaging/gradtables`, and is automatically set from one of those files when a value is entered for `gcoil`.

Values: 18, 31, 33, 40 (nominal, in cm).

Related:
`creategtable` Generate new gradient calibration file (M)
`gcoil` Current gradient coil (P)
`gmax` Maximum gradient strength (P)

sysgcoil	System gradient coil (P)
trise	Gradient rise time (P)

gcoil **Current gradient coil**

Description: Reserved parameter that specifies which physical gradient set is currently installed. This allows convenient updating of important gradient characteristics when one gradient set is interchanged for another. When set, `gcoil` reads the gradient table file of the same name in `/vnmr/imaging/gradtables` and sets the gradient calibration parameters.

`gcoil` is local to each individual experiment. It is normally set the same as `sysgcoil` for acquiring new data, but can be set to other gradient names when working with saved data or data from another instrument. Each possible gradient name should have an associated file of that name located in the directory `/vnmr/imaging/gradtables`. Look at any file in this directory for an example of the proper `gradtable` format, or use the macro `creategtable` to make new `gradtables` entries.

If the parameter `gcoil` does not exist in a parameter set and a user wants to create it, the protection bit that causes the macro `_gcoil` to be executed when the value for `gcoil` is changed must be set. There are two ways to create `gcoil`:

- Use the macro `updtgcoil`, which will create the `gcoil` parameter if it does not exist and set the protection bits.
- Enter the following commands:

```
create('gcoil','string')
setprotect('gcoil','set',9)
```

`gcoil` and the associated gradient calibration parameters `boresize`, `gmax`, and `trise` are updated with the values listed in the table on the right each time a parameter set is retrieved, or when an experiment is joined. In the rare case that a `gradtables` file is modified, but the value of `gcoil` is not changed, manually force an update of the calibration parameters. Updating may be accomplished either by setting `gcoil` to itself, for example, `gcoil=gcoil`, or by using the macro `_gcoil`.

Variable Name	*Value*
boresize	22.50 cm
gmax	5.00 gauss/cm
trise	0.000500 sec

Be aware that if an old dataset is returned and processed, gradient parameters associated with that dataset will replace any new `gcoil` *parameters.*

The table above is a gradient table (gradient coil name: asg33) for a horizontal imaging system with all three axes set to the same maximum gradient strength.

On the right is a gradient table (gradient coil name: tc203) for a three-axis gradient set with unequal maximum gradient strength.

Variable Name	*Value*
boresize	5.10 cm
trise	0.000200 sec
gxmax	29.00 gauss/cm
gymax	27.00 gauss/cm
gzmax	70.00 gauss/cm

Related:

boresize	Magnet bore size (P)
creategtable	Generate new gradient calibration file (M)
gmax	Maximum gradient strength (P)

`setgcoil`	Assign sysgcoil configuration parameter (M)
`sysgcoil`	System gradient coil (P)
`trise`	Gradient rise time (P)
`updtgcoil`	Update gradient coil (M)

`gmax` Maximum gradient strength

Description: Allowed maximum gradient level (absolute value). It is one of the calibration entries in a `gradtables` file.

`gxmax`, `gymax`, and `gzmax` are used when the maximum gradient level is different for each axis, which is the case for triple-axis PFG coils.

Values: Number, in gauss/cm.

See also: *VNMR and Solaris Software Installation*

Related:

`boresize`	Magnet bore size (P)
`creategtable`	Generate new gradient calibration file (M)
`gcoil`	Current gradient coil (P)
`gxmax`,`gymax`,`gzmax`	Maximum gradient strength for each axis (P)
`sysgcoil`	System gradient coil (P)
`trise`	Gradient rise time (P)

`gradstepsz` Gradient step size

Description: Maximum gradient DAC value that determines the type of gradient DAC board used in the system, 12-bit or 16-bit. This parameter is used internally to convert gauss/cm gradient levels to the proper hardware DAC level.

Values: Systems with 12-bit DACs (older SISCO spectrometers without gradient waveform capabilities): –2047 to +2047 units, in integer steps. Systems with 16-bit DACs (all UNITY*plus* and beyond, and SISCO spectrometers with gradient waveform capabilities): –32767 to +32767 units, in integer steps.

See also: *VNMR and Solaris Software Installation*

`gxmax,gymax,gzmax` Maximum gradient strength for each axis

Applicability: Systems with three-axis gradients.

Description: Defines the maximum gradient strength for each gradient axis. Values are read in from the selected system gradient table whenever the parameter set is retrieved or the gradient coil defined by `gcoil` has changed. When the values are read in, `gmax` is set to the lowest value of the three.

`gxmax`, `gymax`, and `gzmax` are used instead of `gmax` when the gradients strengths are not equal for each axis. Unequal gradient strengths per axis are generally true for systems with three-axis PFG coils, which have a strong *z* gradient, and may be true for microimaging systems. Horizontal-bore imaging systems usually have gradients set to the same maximum value, and `gmax` can be used.

Values: Number, in gauss/cm, for each parameter.

See also: *Getting Started, VNMR User Programming*

Related:

`creategtable`	Generate system gradient table (M)
`gcoil`	Current gradient coil (P)
`gmax`	Maximum gradient strength (P)

sysgcoil **System gradient coil**

Description: Specially reserved configurational parameter that specifies which physical gradient set is currently installed, and allows convenient updating of important gradient characteristics when one gradient set is interchanged for another. The value to sysgcoil is assigned to the parameter gcoil when joining experiments or retrieving parameter sets.

See also: *VNMR and Solaris Software Installation*

Related:

boresize	Magnet bore size (P)
creategtable	Generate new gradient calibration file (M)
gcoil	Current gradient coil (P)
gmax	Maximum gradient strength (P)
setgcoil	Assign sysgcoil configuration parameter (M)
trise	Gradient rise time (P)

trise **Gradient rise time**

Description: The rise time to maximum gradient strength, measured from 0% to 100%, assuming a constant rise rate. trise is one of the calibration entries required in a gradtables file. Its value should have been set and recorded at time of installation for gradient sets supplied by Varian.

Related:

boresize	Magnet bore size (P)
creategtable	Generate new gradient calibration file (M)
gcoil	Current gradient coil (P)
gmax	Maximum gradient strength (P)
sysgcoil	System gradient coil (P)

Imaging Gradient Parameters

gpe **Phase encode gradient increment**

Description: Value of the change in phase encode gradient level from one phase encode step to the next. More precisely, the product of the parameters gpe and tpe is used internally within the pulse sequence to determine the phase encode gradient increment based on the computed refocusing time for readout and slice selection. gpe depends on the field of view and the phase encode gradient duration according to the expression γ•gpe*tpe*lpe=1 and is set by either the imprep or setgpe macros.

Related:

imprep	Set up rf pulses, imaging and voxel selection gradients (M)
gmax	Maximum gradient strength (P)
gpe2	2nd phase encoding gradient increment (P)
gpe3	3rd phase encoding gradient increment (P)
lpe	Field of view parameter for phase encode in cm (P)
nv	Number of phase encode steps for 1st indirectly detected dim. (P)
setgpe	Set phase encode gradient levels (M)
tpe	Duration of the phase encoding gradient pulse (P)

gpe2 **2nd phase encode gradient increment**

Description: Phase encode gradient increment for 3D or 4D phase encoded applications. gpe2 should be used when a second phase encode gradient is required. For example, 3D volume imaging application would use both gpe and gpe2, as

would a 3D chemical shift imaging experiment (that is, two spatial dimensions plus chemical shift dimension).

Related:	imprep	Set up rf pulses, imaging and voxel selection gradients (M)
	gmax	Maximum gradient strength (P)
	gpe	Phase encoding gradient increment (P)
	gpe3	3rd phase encoding gradient increment (P)
	lpe2	Field of view size for 2nd phase-encode axis (P)
	setgpe	Set phase encode gradient levels (M)
	tpe2,tpe3	Duration of the 2nd and 3rd phase encoding gradient periods (P)

gpe3 — 3rd phase encode gradient increment

Description: Phase encode gradient increment for 3D or 4D phase encoded applications. gpe3 should be used when a third phase encode gradient is required. It is available for use in a 4D CSI experiment (three spatial dimensions, one chemical shift).

Related:	imprep	Set up rf pulses, imaging and voxel selection gradients (M)
	gpe	Phase encoding gradient increment (P)
	gpe2	2nd phase encoding gradient increment (P)
	lpe3	Field of view size for 3rd phase-encode axis (P)
	setgpe	Set phase encode gradient levels (M)
	tpe2,tpe3	Duration of the 2nd and 3rd phase encoding gradient periods (P)

gped — Phase encode dephasing gradient in the EPI sequence (P)

Applicability: Systems with imaging capabilities.

Description: Determines echo position in the phase-encode direction. A blipped gradient phase encodes the signal with respect to the phase-encode direction. gped determines the center of the k-space along the phase-encode direction. gped is usually set so that eff_echo appears at the center of the phase encode dimension, t1.

Related:	eff_echo	Effective echo position in EPI experiments (P)

gro — Readout gradient strength

Description: Controls the level of the readout gradient, if present. imprep sets gro based on its internal algorithm; or use the macro setgro(value), which sets gro to a specific value and updates at and sw. gro, sw, and at are related by the expression sw=γ*lro*gro, but a change in lro does not automatically update gro and sw.

Related:	at	Acquisition time (P)
	gmax	Maximum gradient strength (P)
	gror	Read out dephasing gradient (P)
	imprep	Set up rf pulses, imaging and voxel selection gradients (M)
	lro	Field of view size for readout axis (P)
	setgro	Set readout gradient (M)
	sw	Spectral width in directly directed dimension (P)

groa — Readout gradient adjuster in EPI experiment (P)

Applicability: Systems with echo planar imaging (EPI) capabilities.

Description: Corrects readout gradient imperfections in EPI experiment by adding an offset (G/cm) to the odd readgradient.

Related:

`episet`	Set up parameters for EPI experiment (M)
`grora`	Readout refocusing gradient adjuster in EPI experiment (P)
`tep`	Post-acquisition delay in EPI experiment (P)

`gror` **Read out dephasing gradient**

Description: Controls the level of the readout refocusing gradient when `pilot='n'`. When `pilot='y'`, `gror` is ignored by the pulse sequence, and computed internally. In this case the internal value is printed in the window used to start VNMR.

`gror` is opposite in sign to `gro` for gradient echo experiments (e.g., FLASH), and have the same sign as `gro` for spin-echo experiments (e.g., SEMS).

In general, the time integral for `gror` should be one half the time integral of `gro` in order to place the echo signal in the center of the AT window. Because the refocusing gradient on-time is internally computed in the pulse sequence independent of the acquisition time, `gror` will not be exactly half of `gro`.

Values: Sequence dependent, specified in gauss/cm up to ±`gmax`.

Related:

`gmax`	Maximum gradient strength (P)
`gro`	Read out fractional compensation (P)
`gssr`	Slice selection refocusing gradient (P)
`pilot`	Automatic sequence calculation (P)

`grora` **Readout dephasing gradient adjuster in EPI experiment (P)**

Applicability: Systems with echo planar imaging (EPI) capabilities.

Description: Correction gradient value added to the readout refocusing gradient (G/cm) in EPI experiments to center the echo position in the acquisition window.

Related:

`episet`	Set up parameters in EPI experiment (M
`groa`	Readout gradient adjuster in EPI experiment (P)
`tep`	Post-acquisition delay in EPI experiment (P)

`gss` **Slice selection gradient strength**

Description: Controls the level of the slice-select gradient, if present. `imprep` sets `gss` based on the slice thickness and rf pulse bandwidths; or use `setgss` to update only `gss`.

Values: Number less than ±`gmax`, in gauss/cm.

Related:

`gmax`	Maximum gradient strength (P)
`gssf`	Slice selection fractional gradient (P)
`gssr`	Slice selection refocusing gradient (P)
`imprep`	Set up rf pulses, imaging and voxel selection gradients (M)
`setgss`	Select slice or voxel selection gradient levels (M))
`thk`	2D imaging plane slice thickness (P)

`gssf` **Slice selection fractional refocusing**

Description: Fractional multiplier used as a fine tuning adjustment for the `gssr` slice refocusing gradient level.

Values: 1.0, when the theoretical gradient calculations are correct.

Related:

gss	Slice selection gradient strength (P)
gssr	Slice selection refocusing gradient (P)

gssr **Slice selection refocusing gradient**

Description: Controls the level of the slice-select refocusing gradient when `pilot='n'`. When `pilot='y'`, `gssr` is ignored by the pulse sequence, and internally computed. The internal value is printed in the window used to start VNMR. `gssr` is normally opposite in sign to `gss`.

In general, the time integral for `gssr` should be very close to one half the time integral of `gss` to properly refocus spins that have dephased during the rf slice selection pulse. Because the refocusing gradient on-time is internally computed in the pulse sequence independent of the rf pulse length, `gssr` will not be exactly half of `gss`.

Values: Number, in gauss/cm, up to ±`gmax`. Nominal value is `gssr=-0.5*gss`.

Related:

gmax	Maximum gradient strength (P)
gss	Slice selection gradient strength (P)
gssf	Slice selection fractional gradient (P)
gror	Read out dephasing gradient (P)
pilot	Automatic sequence calculation (P)

gss2,gss3 **Slice selection gradient level**

Description: Predefined parameters for specifying gradient levels for different slice selection events in an imaging pulse sequence.

Related:

gss	Slice selection gradient strength (P)

image **Control phase encoding gradient in EPI experiments (P)**

Applicability: Systems with echo planar imaging (EPI) capabilities.

Description: Turns on and off the phase encoding gradient in EPI experiments. `image` also specifies the number of EPI images to collect in an arrayed experiment.

Values: 0 specifies that the phase encoding gradient is turned off.

1 specifies that the phase encoding gradient is turned on.

Examples: `image=0,1,1,1` collects a set of four EPI images. The first dataset refers to the reference scan.

Localized Voxel Spectroscopy Gradient Parameters

gvox1–gvox3 **Gradient strength for voxel selection**

Description: Voxel-select gradient levels for the first, second, and third dimensions of a voxel in a localized spectroscopy experiment. For example, `imprep` sets `gvox1` based on the corresponding voxel dimension `vox1` and rf pulse bandwidth. For nonoblique voxels, the orientation of `gvox1` lies along one of the three main gradient axes, X, Y, or Z. Oblique angle voxel orientation is also available, and for this reason the name `gvox1` is used instead of `gx`, for example.

Values: Number, in gauss/cm, less than ±`gmax`.

Related:

`gmax`	Maximum gradient strength (P)
`gss`	Slice selection gradient strength (P)
`gx`	Gradient strength for X, Y, and Z gradients (P)
`vox1–vox3`	Voxel dimension (P)

Special Purpose Gradient Parameters

`gcrush` Crusher gradient level

Description: Predefined parameter available for use in setting a crusher gradient level, often paired with the timing parameter `tcrush`.

Related:

`gspoil`	Spoiler gradient level (P)
`tcrush`	Crusher gradient control (P)
`tspoil`	Gradient spoiling time (P)

`gdiff` Diffusion gradient level

Description: Predefined parameter available for use in setting a diffusion gradient level, often paired with the timing parameters `tdiff` or `tdelta`.

Related:

`tdelta`	Control diffusion sensitizing gradient pulse length (P)
`tDELTA`	Control separation of two diffusion sensitizing gradient pulses (P)
`tdiff`	Diffusion sensitizing gradient pulse length control (P)

`gflow` Flow encoding gradient level

Description: Predefined parameter available for use in setting a flow encoding gradient level, often paired with the timing parameter `tflow`.

Related:

`tflow`	Pulse length control (P)

`gpat–gpat3` Gradient shape

Description: Predefined string parameters available to specify gradient shapes.

`gpepat` Phase-encode gradient shape

Description: Predefined string parameter to specify a phase-encode gradient shape.

`gropat` Readout gradient shape

Description: Predefined string parameter to specify a readout gradient shape.

`gspoil` Spoiler gradient level

Description: Predefined parameter to set a spoiler gradient level. It is often paired with the timing parameter `tspoil`.

Related:

`tcrush`	Crusher gradient control (P)
`tspoil`	Spoiling gradient control (P)

`gsspat` Slice-select gradient shape

Description: Predefined string parameter to specify a slice-select gradient shape.

gtrim **Trim gradient level**

Description: Predefined parameter to set a trim gradient level.

Timing and Delay Parameters

A predefined group of timing and delay parameters is present in all imaging parameter sets, covering the range of most imaging and localized spectroscopy applications. All of these parameters have units of seconds, and are created in VNMR as delay-type parameters The parameter names generally start with either the letter *t*, such as `te` and `tr`, or *d*, such as `d1` and `d2`; the first letter has no particular significance. The names have been selected to correspond as much as possible with common literature usage, but some variation in usage occurs from sequence to sequence, particularly for names with no standard literature definition, such as `tcrush` and `tspoil`.

It is common within a pulse sequence to use a timing or delay parameter to compute one or more "internal" delays that are then used directly to control sequence timing. As an example, `te` is never directly found as an argument to the pulse sequence statement `delay`. Instead, `te` is used to determine smaller delays and events whose sum results in the requested `te`. However, there is no general rule regarding which parameter is directly used and which is indirectly used in internal calculations.

d1 **First delay**

Description: Length of the first delay in the standard two-pulse sequence and most other pulse sequences. This delay is used to allow recovery of magnetization back to equilibrium, if such a delay is desired.

Values: On *MERCURY* systems: 0, 0.2 µs to 150,000 sec. On *GEMINI 2000* systems: 0 to 4095 sec, smallest value possible is 0.2 µs, finest increment possible is 0.1 µs. On systems with a Data Acquisition Controller board: 0 to 8190 sec, smallest value possible is 0.1 µs, finest increment possible is 12.5 ns. On systems with a Pulse Sequence Controller or Acquisition Controller board: 0 to 8190 sec, smallest value possible is 0.2 µs, finest increment possible is 25 ns. On systems with an Output board: 0 to 8190 sec, smallest value possible is 0.2 µs, finest increment possible is 0.1 µs. (Refer to `acquire` statement in the manual *VNMR User Programming* for a description of these boards.)

Related:		
	`alfa`	Set `alfa` delay before acquisition (P)
	`d2`	Incremented delay in 1st indirectly detected dimension (P)
	`d3`	Incremented delay in 2nd indirectly detected dimension (P)
	`pad`	Preacquisition delay (P)

hold **Post-trigger delay**

Description: Delay parameter for specifying a hold time between an external trigger and the start of the actual pulse sequence events.

For example, in cardiac triggered imaging, `hold` provides a mechanism for offsetting the start of the sequence by a variable amount to obtain images at different times in the cardiac cycle.

See also: *VNMR Pulse Sequences*

Related:		
	`ticks`	Number of trigger pulse (P)
	`xgate`	Load time counter (P)

pad — **Preacquisition delay**

Description: Each NMR experiment starts with a single delay time equal to `pad` over and above the delay `d1` that occurs before each transient. Normally, `pad` is set to a small, nominal time (0.5 seconds) to allow any hardware changes that may be required at the start of the acquisition to “settle in.” During experiments in which the temperature is changed, the acquisition starts `pad` seconds after the temperature regulation system comes to regulation. Since the sample temperature does not actually come to equilibrium for some time after that, it is generally desirable to increase `pad` to perhaps 300 seconds. This is especially true when running experiments involving arrays of temperatures. The `pad` parameter is most useful for running kinetics experiments. For example, `pad=0,3600,3600,3600,3600` will run an experiment immediately when `go` is typed (`pad=0`), then wait an hour (3600 seconds), run the second experiment, etc.

Values: On *GEMINI 2000* systems: 0 to 4095, in seconds.
On systems other than *GEMINI 2000*: 0 to 8190, in seconds.

Related:

`d1`	First delay (P)
`go`	Submit experiment to acquisition (C)

tau–tau2 — **Delay**

Description: Predefined delays for general purpose use in imaging sequences. These delays are also used in solid-state experiments.

tcrush — **Crusher gradient control**

Description: Delay parameter for use in controlling a crusher gradient. For example, `tcrush` is used in the MEMS sequence to control the pair of gradient events that destroy coherent magnetization from unwanted stimulated echoes.

Related:

`gcrush`	Crusher gradient level (P)
`gspoil`	Spoiler gradient level (P)
`tspoil`	Gradient spoiling time (P)

tdelta — **Control diffusion sensitizing gradient pulse length**

Description: Timing parameter to control the length of a diffusion sensitizing gradient pulse. Most diffusion weighted imaging sequences use a pair of gradient pulses to achieve contrast based on diffusion, each of length `tdelta`. The separation in time between these gradient pulses is normally defined as `tDELTA`, in an attempt to correspond to the original definitions of Stejkal and Tanner (δ and Δ).

Related:

`gdiff`	Diffusion gradient level (P)
`tDELTA`	Control separation of two diffusion sensitizing gradient pulses (P)
`tdiff`	Diffusion sensitizing gradient pulse length control (P)

tDELTA — **Control separation of two diffusion sensitizing gradient pulses**

Description: Timing parameter to control the separation of a pair of diffusion sensitizing gradient pulses. Most diffusion weighted imaging sequences use a pair of gradient pulses to achieve contrast based on diffusion, each of length `tdelta`. The separation in time between these gradient pulses is normally defined as

tDELTA, in an attempt to correspond to the original definitions of Stejkal and Tanner (δ and Δ).

Related:	gdiff	Diffusion gradient level (P)
	tdelta	Control diffusion sensitizing gradient pulse length (P)
	tdiff	Diffusion sensitizing gradient pulse length control (P)

tdiff — Diffusion sensitizing gradient pulse length control

Description: Timing parameter available to control the length of a diffusion sensitizing gradient pulse. Standard Varian pulse sequences more commonly use the parameter tdelta for this purpose.

Related:	gdiff	Diffusion gradient level (P)
	tdelta	Control diffusion sensitizing gradient pulse length (P)
	tDELTA	Control separation of two diffusion sensitizing gradient pulses (P)

te — Echo time

Description: Echo time for imaging and some localized spectroscopy experiments.

For gradient and spin echo imaging sequences, te is usually defined as the time measured from the middle of the initial rf excitation pulse to the center of the resulting echo. In multiecho sequences, te also defines the time duration between successive echoes, which is normally a constant interval. Multiecho sequences with variable echo times are also possible, in which case the te period between successive echoes may take on a range of values represented by a te array.

Some more unusual pulse sequences, such as stimulated echo, RARE and Fast Spin Echo, use te in ways somewhat different from the previously described normal standards. Consult the descriptions in Chapter 2, “Imaging Experiments,” for specific definitions of te in these applications.

Related:	ne	Number of echoes to be acquired (P)

tep — Post-acquisition delay in EPI experiments (P)

Applicability: Systems with echo planar imaging (EPI) capabilities.

Description: Delay used in the EPI sequence to adjust the beginning of data acquisition. This correction is necessary to allow for the finite (propagation) delay of gradient pulses. This allows the user to center the EPI echoes in the acquisition window.

Values: Number, in µs. Typically 0 to 50 µs, depending on the gradient hardware.

Related:	episet	Set up parameters for EPI experiment (M)

tflow — Pulse length control

Description: Timing parameter to control the length of a flow sensitizing gradient pulse.

Related:	gflow	Flow encoding gradient level (P)

ti — Inversion recovery time

Description: Recovery time following an inversion prepulse in inversion recovery experiments. ti generally has a strong impact on image contrast, which

depends on the T_1 relaxation time of the sample in different regions of the image.

Related:

ir	Inversion recovery mode (P)
pi	Width of an inversion pulse (P)
pipat	Shape of an inversion pulse (P)
tpwri	Inversion pulse power (P)

tm **Stimulated echo mixing time**

Description: Time period in stimulated echo sequences between the second and third rf pulses. tm is also used in the ISIS pulse sequence to specify the time between the last selective inversion pulse and the excitation pulse.

tpe **Duration of the phase encoding gradient pulse**

Description: The length of the phase encoding gradient period in imaging and CSI experiments. sw1, the spectral width in the indirect dimension, is determined from tpe as sw1=1/tpe. tpe can be recomputed within the pulse sequence to provide optimum performance, such as minimum echo time, or scaled to match the required timing for slice refocusing and readout dephasing.

Related:

gpe	Phase encoding gradient increment in DAC units (P)
nv	Number of phase encode steps for 1st indirectly detected dim. (P)
sw1	Spectral width in 1st indirectly detected dimension (P)
tpe2,tpe3	Duration of 2nd and 3rd phase encoding gradient periods (P)

tpe2,tpe3 **Duration of 2nd and 3rd phase encoding gradient periods**

Description: Lengths of the phase encoding gradient periods that control second spatial and third spatial dimensions in higher dimensional imaging and CSI experiments.

As an example, three-dimensional volume imaging sequence have two independent phase encode axes, controlled by tpe and tpe2. It is common to have a single phase encoding time block, in which two independent phase encode gradients share the same time period. In this case, tpe and tpe2 would be equal.

Related:

nv2	Number of phase encode steps for 2nd indirectly detected dim. (P)
nv3	Number of phase encode steps for 3rd indirectly detected dim. (P)
sw2	Spectral width in 2nd indirectly detected dimension (P)
tpe	Duration of the phase encoding gradient pulse (P)

tr **Repetition time in imaging and localized spectroscopy experiments**

Description: Repetition time of an experiment. The definition of repetition time can vary somewhat from pulse sequence to pulse sequence. In general, for imaging experiments, tr is the time required to complete one transient of one phase encode step, including relaxation delay, excitation, data acquisition, and any post-acquire events, such as rf spoiling, phase encode rewinding, and gradient turn-off.

For multislice and/or multiecho imaging sequences, tr includes the complete multslice and multiecho train (for standard arrayed slice acquisitions, where the second character in seqcon is s, the complete train is not included, and tr is the repetition time for each slice position).

Some 1D experiments, such as STEAM and ISIS are also written using tr, with the similar definition that tr is the repetition time per transient.

tr describes the total duration of all events in a pulse sequence, and is never directly found as an argument to “delay.” Instead, tr is generally used in precalculations to determine the time required to pad the sum of programmed events up to the desired repetition time. This padding delay is often found in the pulse sequence as “predelay.”

Related: seqcon — Acquisition loop control (P)

trelax **Relaxation delay**

Description: Timing parameter to specify a relaxation delay. A common use for trelax would be as the inter-image delay in a series of fast images.

tspoil **Gradient spoiling time**

Description: Delay parameter for use in controlling a spoiling gradient. Many imaging sequences use tspoil to set the additional time that the slice-select gradient is on, symmetrically bracketing the 180° refocusing pulse, to spoil any magnetization excited by the 180 itself.

Related:	gcrush	Crusher gradient level (P)
	gspoil	Spoiler gradient level (P)
	tcrush	Crusher gradient control (P)

RF Pulse Lengths, Pulse Power Levels, Shaped Pulse Patterns

The predefined rf pulse parameters have been chosen to cover the majority of imaging and localized spectroscopy applications. In most cases, a trio of related parameters are available, specifying the pulse length, the associated power level, and an rf waveform shape if required. An example is the “parameter group” p1, tpwr1, and p1pat. These are, in fact, three independent parameters, and there is no hard rule that requires them to be associated. It is convenient to write a pulse sequence so that, for example, the power level for pulse p1 is tpwr1, and the parameter specifying the shape of p1 is named p1pat. Standard Varian imaging sequences are written in an attempt to have pulse names follow the obvious progression of the sequence, and where possible to use names that are descriptive of their function. For example, an inversion recovery spin-echo sequence would start with an inversion pulse of length pi (with a power level specified by tpwri and pattern specified by pipat), followed by the 90° slice selective excitation pulse (p1, tpwr1, p1pat), and ending with the 180° refocusing pulse (p2, tpwr2, p2pat).

All pulse length parameters are defined in VNMR as type “pulse,” meaning that pulse durations are entered in µs. The standard limit on maximum pulse length is 8190 µs. Use the setlimit command to increase the upper limit on length. Remember that pulse durations are internally converted to seconds for purposes of pulse sequence calculations (refer to the manuals *VNMR Command and Parameter Reference* and *VNMR User Programming* for more detailed information).

The predefined pulse power parameters have maximum and minimum values derived from the global configuration parameters parmax and parmin. These limits are specified during the initial system configuration process (see the command config) and depend on the system hardware. Power levels are integer values, on a logarithmic dB scale (on VXR and UNITY generation SISCO systems, a unit change in a power-level parameter corresponds to a 0.5-dB change in output power). Pulse power levels are controlled by

selecting a variable level of attenuation at the output of the transmitter. The minimum power level (not necessarily zero on all systems) does not result in zero transmitter output, but simply minimum output, which depends on the attenuator range.

Pulse shape parameters are string parameters that may be used to hold the name of an rf pattern file found in a local or system `shapelib`. Pulse sequences are generally written using these shape parameters, instead of hard-coding the shape names, to allow the pulse shapes to be changed conveniently in the parameter set from the command line or a macro.

Pulse Length Parameters

`pw`, `p1–p5` Pulse length

Description: General purpose rf pulse length parameters, used to specify pulse durations where a descriptive name is not required.

Definition and usage will vary from sequence to sequence. Standard Varian imaging sequences use pulse labels in ascending numerical order to correspond with rf pulses as they occur in the timeline of sequence events.

Values: Number, in µs.

Related:

`pwpat,p1pat–p5pat`	Pulse shape (P)
`tpwr–tpwr5`	Pulse power levels (P)

`pi` Inversion pulse length

Description: Pulse length for an inversion pulse, often used as an optional first pulse preceding the main sequence to provide contrast based on T_1 relaxation. A `pi` pulse is often programmed so that it can be toggled on or off by the user with the inversion-recovery flag `ir`.

Related:

`ir`	Inversion recovery mode (P)
`pipat`	Inversion pulse shape (P)
`ti`	Inversion recovery time (P)
`tpwri`	Inversion pulse power (P)

`pmt` Magnetization pulse length

Description: Pulse length for a magnetization transfer pulse, often used as an optional first pulse preceding the main sequence to provide magnetization-transfer contrast.A `pmt` pulse is often programmed so that it can be toggled on or off by the user with the flag `mt`.

Related:

`mt`	Magnetization transfer on/off (P)
`mtpat`	Magnetization transfer pulse rf shape (P)
`mtpwr`	Magnetization transfer pulse power level (P)

`psat` Saturation pulse length

Description: Pulse length for a saturation pulse, often used as an optional first pulse preceding the main sequence to provide water, fat, or solvent suppression. A `psat` pulse is often programmed so that it can be toggled on or off by the user with the flags `ws` or `presat`.

Related:

`presat`	Presaturation pulse execution on/off (P)
`satfrq`	Presaturation frequency (P)
`satpat`	Presaturation pulse rf shape (P)

`satpwr`	Saturation/presaturation pulse power level (P)
`ws`	Water suppression (P)
`wsfrq`	Specify water suppression frequency (P)

Pulse Power Parameters

`dpwr–dpwr5` **Power levels for second channel events**

Description: General purpose rf decoupler power parameters, used to specify power levels for events on a second channel.

Refer to the *VNMR Command and Parameter Reference* for information about the additional use of these parameters in nonimaging applications.

Related:

`decpat–decpat5`	Pulse shape (P)
`tpwr–tpwr5`	Power level of obs. transmitter with lin. amp. (P)

`mtpwr` **Magnetization transfer pulse power level**

Description: Pulse power level for magnetization transfer pulse.

Related:

`mt`	Magnetization transfer on/off (P)
`mtpat`	Magnetization transfer pulse rf shape (P)
`pmt`	Magnetization pulse length (P)

`satpwr` **Saturation/presaturation pulse power level**

Description: Pulse power level for saturation or presaturation pulse.

Related:

`psat`	Saturation pulse length (P)
`presat`	Presaturation pulse execution on/off (P)
`satpat`	Presaturation pulse rf shape (P)

`tpwr–tpwr5` **Pulse power levels**

Description: General purpose rf power parameters, used to specify pulse power levels where a descriptive name is not required. Definitions and usages vary from sequence to sequence, but generally, names for pulse powers and lengths correspond, for example, `tpwr2` usually describes the power level for pulse `p2`.

Related:

`pw,p1–p5`	Pulse length (P)
`pwpat,p1pat–p5pat`	Pulse shape (P)

`tpwri` **Inversion pulse power level**

Description: Pulse power level for an inversion pulse. It specifies the peak power of transmitter pulses corresponding to `pi`.

Related:

`ir`	Inversion recovery mode (P)
`pi`	Inversion pulse length (P)
`pipat`	Inversion pulse shape (P)
`ti`	Inversion recovery time (P)

Pulse Shape Parameters

decpat–decpat5 **Pulse shape**

Description: General purpose rf decoupler parameters used to specify pulse shapes for pulses on a second rf channel.

Related: dpwr–dpwr5 Power levels for second channel events (P)

mtpat **Magnetization transfer pulse rf shape**

Description: Holds the name of the rf shape used for a magnetization transfer pulse.

Related:	mt	Magnetization transfer on/off (P)
	mtpwr	Magnetization transfer pulse power level (P)
	pmt	Magnetization pulse length (P)

pwpat,p1pat–p5pat **Pulse shape**

Description: General purpose string parameters used to specify rf pulse shape names when a descriptive name is not required. Definitions and usages vary from sequence to sequence, but there is a general correspondence between names for pulse shapes, for example, p2pat is commonly used to describe the shape name for pulse p2.

Related:	pw,p1–p5	Pulse length (P)
	tpwr–tpwr5	Pulse power levels (P)

pipat **Inversion pulse shape**

Description: Holds the name of the rf shape used for inversion pulse pi.

Related:	ir	Inversion recovery mode (P)
	pi	Inversion pulse length (P)
	ti	Inversion recovery time (P)
	tpwri	Inversion pulse power level (P)

satpat **Presaturation pulse rf shape**

Description: Holds the name of the rf shape used for a presaturation pulse.

Related:	presat	Presaturation pulse execution on/off (P)
	psat	Saturation pulse length (P)
	satpwr	Saturation/presaturation pulse power level (P)

Dimensions, Positions, and Orientations

The predefined field-of-view (FOV) parameters cover the majority of all imaging and localized spectroscopy applications in common use. A number of these parameter names are expected by certain VNMR functions, and it is advisable to retain these names to avoid any incompatibilities. For example, the dconi (or imconi) program gets the dimensions for axis display from the parameters lro and lpe.

Units for the dimensional and positional parameters are in cm and mm, depending on the particular parameter. In general, image FOV and slice and readout positions have units of cm. Slice thickness and voxel dimensions for localized spectroscopy have units of mm. Dimension and position parameters are created in VNMR as standard real-type parameters, with no special limits.

Orientation of an imaging plane is specified through a set of three Euler angle parameters. The user normally does not directly set these Euler angle parameters, but instead controls

the orientation of the imaging plane through the parameter `orient` or through interactive graphical planning of new imaging orientations.

Image Field-of-View and Orientation Parameters

`lpe` Field of view size for phase encode axis

Description: The size of the image field of view along the phase-encode dimension. `lpe` is used by `dconi` (and `imconi`) to specify the phase-encode axis dimensions when the `axis` parameter is set to positional units of cm or mm.

To change `lpe`, enter the desired value through the VNMR command line, and then run `imprep` to update other dependent parameters. `lpe`, `gpe`, and `tpe` are related by the expression γ*`lpe*tpe*gpe=1`.

Values: Number, in cm.

Related:

`axis`	Axis label for displays and plots (P)
`dconi`	Interactive 2D contour display (C)
`gpe`	Phase encoding gradient increment (P)
`imconi`	Display 2D data in interactive gray-scale mode (M)
`imprep`	Set up rf pulses, imaging, and voxel selection gradients (M)
`lro`	Field of view size for readout axis (P)
`setgpe`	Set phase encode gradient levels (M)
`sw1`	Spectral width in 1st indirectly detected dimension (P)
`tpe`	Duration of the phase encoding gradient pulse (P)

`lpe2` Field of view size for 2nd phase-encode axis

Description: The size of the field of view along a second phase-encode dimension. Higher order phase-encode dimensions are found in 3D volume imaging, and Chemical Shift Imaging (CSI) experiments with two spatial dimensions.

Values: Number, in cm.

Related:

`gpe2`	2nd phase encoding gradient increment (P)
`imprep`	Set up rf pulses, imaging, and voxel selection gradients (M)
`lpe3`	Field of view size for 3rd phase-encode axis (P)
`seqcon`	Acquisition loop control (P)
`setgpe`	Set phase encode gradient levels (M)
`sw2`	Spectral width in 2nd indirectly detected dimension (P)
`tpe`	Duration of the phase encoding gradient pulse (P)

`lpe3` Field of view size for 3rd phase-encode axis

Description: The size of the field of view along a third phase-encode dimension. Higher order phase-encode dimensions are found in Chemical Shift Imaging (CSI) experiments with three spatial dimensions.

Values: Number, in cm.

Related:

`gpe3`	3rd phase encoding gradient increment (P
`imprep`	Set up rf pulses, imaging, and voxel selection gradients (M)
`lpe2`	Field of view size for 2nd phase-encode axis (P)
`seqcon`	Acquisition loop control (P)
`setgpe`	Set phase encode gradient levels (M)
`sw3`	Spectral width in 3rd indirectly detected dimension (P)
`tpe`	Duration of the phase encoding gradient pulse (P)

`lro` **Field of view size for readout axis**

Description: The size of the image field of view along the readout dimension. This parameter is used by `dconi` (and `imconi`) to specify the readout axis dimensions when the axis parameter is set to positional units of cm or mm.

To change `lro`, enter the desired value through the VNMR command line, and then run the macro `imprep` to update other dependent parameters. `lro`, `sw`, and `gro` are related by the expression `sw=γ*lro*gro`.

Values: Number, in cm.

Related:

`axis`	Axis label for displays and plots (P)
`dconi`	Interactive 2D contour display (C)
`gro`	Readout gradient strength (P)
`imconi`	Display 2D data in interactive gray-scale mode (M)
`imprep`	Set up rf pulses, imaging, and voxel selection gradients (M)
`lpe`	Field of view size for phase-encode axis (P)
`setgro`	Set readout gradient (M)
`sw`	Spectrum width (P)

`orient` **Slice plane orientation**

Description: The orientation of an imaging plane, volume, or projection in the magnet reference frame.The allowed settings of orient are `trans`, `cor`, `sag`, and `oblique`, corresponding to transverse (Z slice plane), coronal (Y slice plane), and sagittal (X slice plane). `trans`, `cor`, and `sag` are the three “major” orientations, that is, they have readout, phase-encode, and slice selection axes that are combinations of the three major X, Y, and Z laboratory frame axes.

.The table on the right lists the complete descriptions of the three major orientations

Orientation	*Readout*	*Phase Encode*	*Slice Select*
trans	Y	X	Z
cor	Z	X	Y
sag	Z	Y	X

An oblique orientation is angled so that it does not correspond to one of the three major planes. The frame of reference for imaging orientation is the magnet bore, with the Z axis lying along the bore. For a horizontal bore magnet, the X and Z axes are parallel to the floor, with Y in the vertical direction. For a vertical bore magnet Z lies along the bore in the vertical direction, with X and Y parallel to the floor. X and Y orientation in a vertical system depends on the rotational position of the gradient set.

`orient` is a convenient way to specify imaging plane orientation, but underlying `orient` are three additional parameters that explicitly control the orientation. These are the Euler angle parameters `psi`, `phi`, and `theta`, which are used to precisely set the imaging plane to any arbitrary major or oblique orientation, and to communicate this information to the pulse sequence. Two of these Euler angle parameters, `psi` and `theta`, determine the orientation of a vector that is perpendicular to the desired imaging plane (the slice position `pss` specifies the distance from the origin to the imaging plane along this vector). `theta` is the angle between this vector and the magnet Z axis. `psi` is the angle between the projection of this vector onto the magnet XY plane, and the magnet

Y axis. The third angle, `phi`, determines the rotational orientation of the imaging plane about the psi-theta vector.

The table on the right lists the three major orientations specified by these combinations of `phi`, `psi`, and `theta`.

Orientation	*theta*	*psi*	*phi*
trans	0	0	0
cor	90	0	0
sag	90	90	0

Entering `orient='trans'` automatically sets these parameters to the proper values. In all three cases, `phi` is zero, and its function is to rotate the imaging plane about the orientation vector. Thus, to reverse the readout and phase-encode axes in an image, set `phi` to 90 instead of 0.

The three major imaging plane orientations are unique in their combinations of `psi`, `phi`, and `theta`, and so can be easily represented with the designations transverse, coronal, and sagittal. Orientations that do not lie in one of these major planes are "oblique," and have at least one of the Euler angle parameters set to a value other than 0 or 90. Since there are a nearly limitless number of oblique orientations, any nonmajor orientation has have `orient` set to `'oblique'`, indicating only that the Euler angle parameters describe a nonmajor plane.

Setting `orient='oblique'` does not determine a unique orientation, so instead there are two mechanisms for specifying oblique planes. The first is to enter a value of `psi`, `phi`, or `theta` that does not specify one of the major imaging planes, for example `theta=45`. The second is to follow the interactive planning procedure that allows graphical setup of imaging orientation from an existing scout image. Either of these procedures automatically set `orient` to `'oblique'`.

Values: `'trans'`, `'sag'`, `'cor'`, `'oblique'`

Related:

`dorient`	Diffusion gradient orientation (P)
`orient2`	Other orientation (P)
`phi`	Euler angle for defining imaging plane orientation (P)
`plan`	Display menu for planning a target scan (M)
`psi`	Euler angle for defining imaging plane orientation (P)
`pss`	Slice position (P)
`sorient`	Saturation band gradient orientation (P)
`theta`	Euler angle for defining imaging plane orientation (P)
`vorient`	Voxel orientation (P)

phi — Euler angle for defining imaging plane orientation

Description: One of the three Euler angles used to define imaging plane orientation. `phi` determines the angular rotation of the image plane about a line normal to the image plane. `phi` is generally not set directly by the user, but instead either by entering a string value into the `orient` parameter or through interactive graphical planning of a new imaging plane from an existing scout image. `phi` can be used to rotate the readout axis into the phase-encode axis, and vice-versa. To do this, add (or subtract) 90 to the current value of `phi`.

Values: –180 to +180, in degrees.

Related: `orient` Slice plane orientation (P)

`psi`	Euler angle for defining imaging plane orientation (P)
`theta`	Euler angle for defining imaging plane orientation (P)

`pro` **Position of image center on the readout axis**

Description: The readout position measured from the gradient coordinate origin. `pro` is independent of imaging plane orientation, and is the distance from the gradient origin to the center of the image along the readout direction. `pro` is used by most imaging pulse sequences as an argument to the `poffset` function, which internally computes the spectrometer frequency required to center the readout axis at the value of `pro`. The value of `pro` can be entered manually, or graphically with `movepro`.

Values: Number, in cm.

Related:

`lro`	Field of view size for phase encode axis (P)
`movepro`	Move the imaging readout position (C)
`resto`	NMR resonance offset frequency (P)

`psi` **Euler angle for defining imaging plane orientation**

Description: One of the three Euler angles used to define imaging plane orientation. `psi` is the angle formed by the projection of a line normal to the imaging plane onto the magnet XY plane, and the magnet Y axis. `psi` is generally not set by the user directly, but instead either by entering a string value into the `orient` parameter, or through interactive graphical planning of a new imaging plane from an existing scout image.

Values: –90 to +90, in degrees.

Related:

`orient`	Slice plane orientation (P)
`phi`	Euler angle for defining imaging plane orientation (P)
`theta`	Euler angle for defining imaging plane orientation (P))

`pss` **Slice position**

Description: Slice position measured from the gradient coordinate origin. `pss` is independent of imaging plane orientation and is the distance from the gradient origin to the desired imaging slice along the imaging plane orientation vector. It can be arrayed to specify a list of slice positions for a multislice imaging experiment. Most multislice sequences acquire data following the order of slice positions found in `pss`. A monotonic list of positions, for example, `pss=1,2,3,4,5,6`, results in multislice excitation in that order.

To get interleaved slice excitation order (e.g., 1,3,5,2,4,6), `pss` should be arrayed exactly as desired, for example, `pss=1,3,5,2,4,6`. The number of slices in a multislice experiment is determined by the number of arrayed elements in `pss`, and is displayed in the parameter `ns`, which cannot be directly entered, and only reflects the number of values found in the `pss` array. To increase or decrease the number of slices, `pss` must be changed or reentered, after which `ns` is automatically updated. Although `pss` is an acquisition parameter, arraying it does not normally result in a conventional “arrayed” experiment.

When `seqcon` is set to specify multislice acquisition in compressed mode, `pss` protection bit 8 is turned on, turning off the automatic arrayed experiment feature. In this case, the values of `pss` are read into the pulse sequence and used in the `poffset_list` (or `position_offset_list`) pulse sequence

statements to specify the list of slice positions. For this reason, the `da` command does not normally display the values contained in a `pss` array. To see this list of values enter the command `da('pss')`.

Values: Number, in cm.

Related:

`da`	Display acquisition parameter arrays (C)
`gss`	Slice selection gradient strength (P)
`ns`	Number of slices to be acquired (P)
`seqcon`	Acquisition loop control (P)
`sliceorder`	Reorder the slice position list (M)
`thk`	Slice thickness (P)

`theta` **Euler angle for defining imaging plane orientation**

Description: One of the three Euler angles used to define imaging plane orientation. `theta` is the angle formed by the line normal to the imaging plane, and the magnet Z axis. `theta` is generally not directly set by the user, but instead set either by entering a string value into the `orient` parameter or through interactive graphical planning of a new imaging plane from an existing scout image.

Related:

`orient`	Slice plane orientation (P)
`phi`	Euler angle for defining imaging plane orientation (P)
`psi`	Euler angle for defining imaging plane orientation (P)

`thk` **Slice thickness**

Description: Slice thickness for a 2D imaging plane or 3D slab selection. To change `thk`, enter the desired value through the VNMR command line, and then run the macro `imprep` to update other dependent parameters. `thk` and `gss` are related by the expression `gss=10*BW/(γ*thk)` where `BW` is the bandwidth of the rf pulse used for slice selection.

Values: Number, in mm.

Related:

`gss`	Slice selection gradient strength (P)
`imprep`	Set up rf pulses, imaging, and voxel selection gradients (M)
`setgss`	Select slice or voxel selection gradient levels (M)

Voxel Dimension, Position, and Orientation Parameters

`pos1–pos3` **Position of voxel center**

Description: Voxel position measured from the gradient coordinate origin. `pos1`, `pos2`, and `pos3` are independent of voxel orientation and are the distances from the gradient origin to the center of the desired voxel along the three axes of the rotated coordinate frame specified by the voxel orientation. Voxel positions are most often be determined through the interactive voxel planning procedure from a scout image, but can be entered manually through the command line.

The voxel position ultimately used during pulse sequence execution, to compute the spectrometer offset frequency required to place the center of the voxel at the correct spatial position in the presence of a voxel selection gradient, is described by the equation:

`offset=resto+γ*pos1*gvox1`.

This simple calculation is the basis for the pulse sequence statement `poffset`. Because the frequency offset is determined internally by the pulse sequence at run time, it is not necessary to run the `imprep` macro after changing `pos1`.

Values: Number, in cm.

Related:

`gvox1–gvox3`	Gradient strength for voxel selection (P)
`imprep`	Set up rf pulses, imaging and pulse power levels (M)
`plan`	Interactive slice and voxel selection (M)
`resto`	NMR resonance offset frequency (P)
`vorient`	Voxel orientation (P)
`vox1–vox3`	Voxel dimensions (P)

`vox1–vox3` Voxel dimensions

Description: Voxel dimension for volume localized experiments. Volume localized experiments (such as STEAM and ISIS) can be oriented so that voxel edges lie parallel to major magnet axes, or edges may have oblique angle orientations relative to major axes. For this reason, parameters that define voxel dimensions do not refer to the X, Y, and Z axes in their names.

Voxel dimensions are most often determined through the interactive voxel planning procedure from a scout image, but can be manually entered through the command line. `imprep` updates other parameters that depend on `vox1`, `vox2`, or `vox3`.

`vox1` and `gvox1` are related by the expression `gvox1=10*BW/(`γ`*vox1)`, in which `BW` is the bandwidth of the rf pulse used for voxel selection (similarly for `vox2` and `vox3`).

Values: Number, in mm.

Related:

`gvox1–gvox3`	Gradient strength for voxel selection (P)
`imprep`	Set up rf pulses, imaging and voxel selection gradients (M)
`plan`	Interactive slice and voxel selection (M)
`pos1–pos3`	Position of voxel center (P)

`vorient` Voxel orientation

Description: Orientation of a voxel in the magnet reference frame, typically in localized single-voxel spectroscopy experiments such as STEAM and ISIS.

`vorient` corresponds in its basic definitions to its sister parameter `orient`, with the substitution of the axis designators “1,” “2,” and “3” for the descriptors “readout,” “phase encode,” and “slice select.” `vorient`, in turn, determines three Euler angle parameters, `vphi`, `vpsi`, and `vtheta`, which are analogs to the `phi`, `psi`, and `theta` parameters. For example, if `vorient='sag'`, `pos1` lies along Z, `pos2` along Y, and `pos3` along X, with voxel Euler angles `vtheta=90`, `vpsi=90`, and `vphi=0`.

Values: `'trans'`, `'sag'`, `'cor'`, `'oblique'`

Related:

`orient`	Slice plane orientation (P)
`plan`	Interactive slice and voxel selection (M)
`pos1–pos3`	Position of voxel center (P)
`vphi`, `vpsi`, `vtheta`	Euler angles for voxel orientation (P)

vphi,vpsi,vtheta **Euler angles for voxel orientation**

Description: Euler angles used to define voxel orientation. Definitions are similar to the imaging plane orientation definition parameters phi, psi, and theta.

Generally, voxel Euler angles are not directly set by the user, but instead are set either by entering a string value into vorient or through interactive graphical planning of a voxel plane from an existing scout image.

Related:

phi	Euler angle for defining imaging plane orientation (P)
psi	Euler angle for defining imaging plane orientation (P)
theta	Euler angle for defining imaging plane orientation (P)
plan	Interactive slice and voxel selection (M)
vorient	Voxel orientation (P)

Special Purpose Orientation Parameters

dorient **Diffusion gradient orientation**

Description: Orientation of a diffusion gradient with respect to the magnet coordinate system. Description and definition is equivalent to vorient.

Related:

dphi,dpsi,dtheta	Euler angles for diffusion gradient orientation (P)
vorient	Voxel orientation (P)

dphi,dpsi,dtheta **Euler angles for diffusion gradient orientation**

Description: Euler angle parameters used to define diffusion gradient orientation. Descriptions and definitions are equivalent to vphi, vpsi, and vtheta.

Related:

dorient	Diffusion gradient orientation (P)
vphi,vpsi,vtheta	Euler angles for voxel orientation (P)

orient2 **Other orientation**

Description: Spare orientation parameter for use in defining the orientation of any gradient other than for diffusion, saturation, slice, or voxel with respect to the magnet coordinate system. Description and definition are equivalent to vorient.

Related:

vorient	Voxel orientation (P)
phi2,psi2,theta2	Euler angles for other orientations (P

phi2,psi2,theta2 **Euler angles for other orientations**

Description: Spare Euler angle parameters. Descriptions and definitions are equivalent to vphi, vpsi, and vtheta.

Related:

orient2	Other orientation (P)
vphi,vpsi,vtheta	Euler angles for voxel orientation (P)

sorient **Saturation band orientation**

Description: Orientation of a saturation band with respect to the magnet coordinate system. Description and definition is equivalent to vorient.

Related:

sphi,spsi,stheta	Euler angles for saturation band orientation (P)
vorient	Voxel orientation (P)

sphi,spsi,stheta **Euler angles for saturation band orientation**

Description: Euler angle parameters used to define saturation band orientation. Descriptions and definitions are equivalent to vphi, vpsi, and vtheta.

Related:

sorient	Saturation band orientation (P)
vphi,vpsi,vtheta	Euler angles for voxel orientation (P)

Frequency Offsets and Spectral Widths

Predefined frequency offset parameters are provided to cover the majority of common applications, such as water suppression, magnetization transfer, or chemical shift selection. All of these frequency parameters have units of Hz, and are created in VNMR as frequency-type parameters.

Most vertical bore microimaging systems have frequency resolution of 0.1 Hz, while most horizontal imaging systems have frequency resolution of 1 Hz. Some pulse sequences may use certain frequency offsets differently than others, that is, in some cases, a frequency offset parameter may be an absolute offset from the base spectrometer frequency, and in other cases it may be a delta, or relative offset, from some other reference frequency.

Frequency Parameters

chessfrq **Chemical shift selective pulse frequency**

Description: Frequency offset parameter for use in specifying the frequency for a chemical shift selective pulse.

Related:

offset	Calculate and display absolute frequency offset at cursor (M)
resto	NMR resonance offset frequency (P)

resto **NMR resonance offset frequency**

Description: Frequency offset used as a chemical shift reference by most imaging and localized spectroscopy sequences, typically set to the offset of the water resonance in biological samples.

Selection of the desired slice or voxel position is accomplished internally by the poffset and poffset_list pulse sequence elements by computing the frequency offset required to excite at a position in space that is the product of the position and the gradient strength used. A chemical shift reference offset resto must be added to this offset, for example:

```
offset=resto+γ*pss*gss
```

As an example, suppose the chemical shift offset for water is 4000 Hz, and the desired slice position is 3 cm from center with a 2 G/cm gradient. The offset required to position the slice 3 cm from the gradient origin is 25,548 Hz (γ*pss*gss=4258*3*2). The 4 kHz water resonance offset must be added to this value to avoid an error of 4.7 mm in the slice position. Thus, resto must be added to the gradient produced offset to give the proper frequency offset 29,548 Hz. (The offset macro may be used to determine the value of resto from a one-dimensional spectrum.)

In samples where more than one chemical shift species exists, such as water and fat in biological samples, there is always some error in spatial positioning of at least one of the chemical species due to the chemical shift difference. The

chemical shift specified by `resto` therefore is most accurately positioned in an image or localized spectroscopy voxel.

Users of vertical bore microimaging system may choose to adjust Z0 to bring the reference chemical shift on resonance, and set `resto=0`. Most horizontal bore imaging systems do not have a Z0 shim adjustment, so this is not an option.

Related:
`gss` Slice selection gradient strength (P)
`offset` Calculate and display absolute frequency offset at cursor (M)
`pss` Slice position (P)

`satfrq` **Presaturation frequency**

Description: Frequency offset parameter for use in specifying the frequency for presaturation.

Related:
`offset` Calculate and display absolute frequency offset at cursor (M)
`presat` Presaturation pulse execution on/off (P)
`resto` NMR resonance offset frequency (P)

`wsfrq` **Water suppression frequency**

Description: Frequency offset parameter for use in specifying the frequency for water suppression.

Related:
`offset` Calculate and display absolute frequency offset at cursor (M)
`resto` NMR resonance offset frequency (P)
`ws` Water suppression (P)

Spectral Width Parameters

The spectral width parameters `sw`, `sw1`, `sw2`, and `sw3` are used somewhat differently in imaging than in analytical high-resolution spectroscopy, because of the addition of gradients and spatial dimensions. Refer to the manual *VNMR Command and Parameter Reference* for more complete descriptions of these parameters and to the definitions here for the small differences to these descriptions as they apply to imaging applications.

`sw` **Spectral width in directly detected dimension**

Description: Total width of the spectrum to be acquired, from one end to the other, as described in the manual *VNMR Command and Parameter Reference*.

In imaging experiments, `sw` is generally used as the direct time axis, associated with the acquisition of an echo or FID in the presence of a readout gradient. The value of `sw` is thus determined by the relationship that includes the readout FOV dimension, and readout gradient strength: `sw=γ*lro*gro`. Because of this dependence, `sw` must be recomputed whenever `lro` or `gro` are changed, which can be accomplished with the `imprep` or `setgro` macros.

Though `sw` has units of Hz, it is most common to display images with spatial axes of cm or mm. The `axis` parameter is used to tell the display routines what units to place on axes, and how to scale the aspect ratio in two-dimensional images for proper representation of an image. However, some aspects of image display (such as cursor positions output by the `mark` command) may be represented in Hz by certain functions or macros.

Values: Number, in Hz.

See also: *Getting Started*

Related:

`at`	Acquisition time (P)
`axis`	Axis label for displays and plots (P)
`imprep`	Set up rf pulses, imaging and voxel selection gradients (M)
`lro`	Field of view size for readout axis
`np`	Number of data points (P)
`setgrad`	Set readout gradient (M)
`sw1`	Spectral width in 1st indirectly detected dimension (P)

`sw1` Spectral width in 1st indirectly detected dimension

Description: Spectral width for the first indirectly detected dimension of a multidimensional image data set, as in conventional analytical spectroscopy.

In imaging, `sw1` is generally a phase-encoding dimension created by stepping through a range of phase encode gradient levels with a constant time gradient pulse (number of steps set by the parameter `nv`), instead of incrementing a delay as in analytical 2D spectroscopy. Because phase encoding is a function of both time and gradient, `sw1` has no real significance (as it generally does in 2D spectroscopy where `sw1=1/d2`) other than to act as an artificial value for use by image display and processing routines. The choice of value for `sw1` is therefore somewhat arbitrary, and is generally set to `1/tpe` by `imprep`.

Even though `d2` is not used as an incremental delay in imaging sequences, its value may in fact be automatically incremental in noncompressed sequences. For this reason, imaging pulse sequences should never use `d2`, unless an incremental delay dependent on the value of `sw1` is specifically required.

Refer to the manual *VNMR Command and Parameter Reference* for information about the additional use of `sw1` in nonimaging applications.

Related:

`d2`	Incremented delay in 1st indirectly detected dimension (P)
`imprep`	Set up rf pulses, imaging and voxel selection gradients (M)
`nv`	Number of phase encode steps for 1st indirectly detected dim. (P)
`sw`	Spectral width in directly detected dimension (P)
`sw2`	Spectral width in 2nd indirectly detected dimension (P)
`sw3`	Spectral width in 3rd indirectly detected dimension (P)
`tpe`	Duration of the phase encoding gradient pulse (P)

`sw2` Spectral width in 2nd indirectly detected dimension

Description: Spectral width for the second indirectly detected dimension of a multidimensional data set, used in 3D volume imaging for the third spatial dimension, or CSI for the second spatial dimension. See `sw1` for description, except that number of phase encode steps is controlled by the parameter `nv2`.

Refer to the manual *VNMR Command and Parameter Reference* for information about the additional use of `sw2` in nonimaging applications.

Related:

`imprep`	Set up rf pulses, imaging and voxel selection gradients (M)
`nv2`	Number of phase encode steps for 2nd indirectly detected dim. (P)
`sw`	Spectral width in directly detected dimension (P)
`sw1`	Spectral width in 1st indirectly detected dimension (P)
`sw3`	Spectral width in 3rd indirectly detected dimension (P)
`tpe2,tpe3`	Duration of 2nd and 3rd phase encoding gradient periods (P)

sw3 **Spectral width in 3rd indirectly detected dimension**

Description: Spectral width for the third indirectly detected dimension of a multidimensional data set, used in 3D CSI (three spatial dimensions, one spectral dimension) for the third spatial dimension. See `sw1` for description, except that number of phase encode steps is controlled by the parameter `nv3`.

Refer to the *VNMR Command and Parameter Reference* for information about the additional use of `sw3` in nonimaging applications.

Related:

`imprep`	Set up rf pulses, imaging and voxel selection gradients (M)
`nv3`	Number of phase encode steps for 3rd indirectly detected dim. (P)
`sw`	Spectral width in directly detected dimension (P)
`sw1`	Spectral width in 1st indirectly detected dimension (P)
`sw2`	Spectral width in 2nd indirectly detected dimension (P)
`tpe2,tpe3`	Duration of 2nd and 3rd phase encoding gradient periods (P)

Experiment Control Parameters

Experiment control parameters can be divided into two classes:

- *Counters* are integer parameters used to specify the number of elements in different acquisition loops, such as the number of phase encode steps in a 2D image or the number of slices in a multislice imaging sequence.
- *Flags* are string parameters used in many pulse sequences to turn on or turn off various optional functions, such as a presaturation pulse or inversion-recovery preparation.

Compressed vs. Arrayed Data Acquisition

Multidimensional experiments are acquired in either *standard* (also called *arrayed*) mode, or *compressed* mode. `ni` is used to control standard acquisitions, and `nf` to control compressed acquisitions. For more information, refer to the parameter `seqcon`.

Experiment Counters

cf **Current FID**

Description: Specifies which FID to operate on when working with multi-FID compressed data. All subsequent operations, such as Fourier transformation, are applied to the selected data block. Individual images from a compressed multislice acquisition, for example, are selected through the `cf` parameter. Setting `cf=3` selects slice number 3 (in the order acquired, not necessarily in position order).

Refer to the manual *VNMR Command and Parameter Reference* for information about the additional use of `cf` in nonimaging applications.

Values: Number, 1 through the value of parameter `nf`.

Related:

`flashc`	Convert compressed 2D data to standard 2D format (C)
`ne`	Number of echoes to be acquired (P)
`nf`	Number of FIDs (P)
`ns`	Number of slices to be acquired (P)

ne **Number of echoes to be acquired**

Description: The number of echoes in a multiecho experiment.

All multiecho acquisitions must be in compressed mode. `ne` is then used as the limit for the echo loop counter in pulse sequences with this capability.

Values: 1 to desired number, in integer steps.

Related:

`cf`	Current FID (P)
`nf`	Number of FIDs (P)
`ns`	Number of slices to be acquired (P)
`seqcon`	Acquisition loop control (P)
`te`	Echo time (P)
`setloop`	Control arrayed and real-time looping (M)

`nf` Number of FIDs

Description: The number of compressed acquisitions in a compressed multidimensional, multislice, or multiecho experiment. `nf` is not normally entered directly, but is set automatically when required through other parameters, such as `ne`, `ns`, or `nv`. The parameter `nf`, together with `np`, governs the total number of points that are acquired during one pass through the pulse sequence code, including all loops. The single requirement is that this number of points be equal to the product `nf*np`.

Refer to the manual *VNMR Command and Parameter Reference* for information about the additional use of `nf` in nonimaging applications.

Values: Positive integer.

Related:

`imprep`	Set up rf pulses, imaging and voxel selection gradients (M)
`ne`	Number of echoes to be acquired (P)
`ni`	Number of increments in 1st indirectly detected dim. (P)
`ns`	Number of slices to be acquired (P)
`nv`	Number of phase encode steps for 1st indirectly detected dim. (P)
`seqcon`	Acquisition loop control (P)
`setloop`	Control arrayed and real-time looping (M)

`ni` Number of increments in 1st indirectly detected dimension

Description: The number of standard increments in the first indirectly detected dimension of a multidimensional acquisition. `ni` is not normally directly entered in imaging experiments. Instead, `nv` to control the number of 2D increments.

Refer to the *VNMR Command and Parameter Reference* for information about the use of `ni` in 2D spectroscopy experiments.

See also: *User Guide: Liquids*

Related:

`imprep`	Set up rf pulses, imaging and voxel selection gradients (M)
`nf`	Number of FIDs (P)
`nv`	Number of phase encode steps for 1st indirectly detected dim. (P)
`seqcon`	Acquisition loop control (P)
`setloop`	Control arrayed and real-time looping (M)

`ns` Number of slices to be acquired

Description: Number of slices in a compressed multislice experiment. The number of slices is determined by the number of arrayed elements in `pss`, and is displayed in `ns`, which cannot be directly entered, and reflects only the number of values found in the `pss` array.

To increase or decrease the number of slices, pss must be changed or re-entered, after which ns is automatically updated. When the multislice control character in seqcon is s, indicating a standard arrayed mode of data acquisition for multiple slices, ns is set to 1. The number of slices can then be determined directly from the pss array.

Values: Number, 1 to desired number, in integer steps.

Related:

cf	Current FID (P)
ne	Number of echoes to be acquired (P)
nf	Number of FIDs (P)
plan	Display menu for planning a target scan (M)
pss	Slice position (P)
seqcon	Acquisition loop control (P)
setloop	Control arrayed and real-time looping (M)

np — Number of data points (P)

Description: Sets number of data points to be acquired. Generally, np is a *dependent* parameter and is calculated automatically when sw or at is changed. If a particular number of data points is desired, np can be entered, in which case at becomes the dependent parameter and is calculated based on sw and np.

Values: On *GEMINI 2000*, np is constrained to be a multiple of 64. Upper limit for np on broadband systems is 128,000, the limit on $^{1}H/^{13}C$ systems is 64,000. These limits can be doubled with the setlimit command if dp='n'.

On *MERCURY*, 64 to 128,000, in steps of 64 (dp does not affect the limit because on *MERCURY* dp is always 'y').

On systems other than the *GEMINI 2000*, np is constrained to be a multiple of 2 (Acquisition Controller or Pulse Sequence Controller board) or a multiple of 64 (Output board). (See the acquire statement in the manual *VNMR User Programming* for a description of these boards.)

Related:

at	Acquisition time (P)
dp	Double precision (P)
setlimit	Set limits of a parameter in a tree (C)
sw	Spectral width in directly detected dimension (P)

nt — Number of transients (P)

Description: Sets the number of transients to be acquired (i.e., the number of repetitions or scans performed to make up the experiment or FID).

Values: 1 to 1e9 (for *MERCURY*, the hardware limits nt to 16e6). For an indefinite acquisition, set nt to a very large number such as 1e9.

nv — Number of phase encode steps for 1st indirectly detected dimension

Description: The number of phase encode steps for the first indirectly detected dimension in a multidimensional imaging or CSI experiment.

In a 2D or 3D image, nv controls the resolution in the second spatial dimension (lpe). In a CSI experiment, nv controls the first spatial dimension (lpe). The lower level parameters ni and nf are automatically set each time a value of nv is entered, through the macro setloop, which uses the seqcon parameter to determine if the acquisition is standard or compressed in the dimension controlled by nv, and appropriately sets either ni or nf. Because nv is

explicitly used in most imaging pulse sequences to specify the number of phase encode steps, the user should never directly set `ni` or `nf`, but instead set `nv`, and let the software automatically assign `ni` and `nf`.

Values: Number greater than 0, usually in powers of 2. Typical values: 0, 64, 128, 256.

Related:

`flashc`	Convert compressed 2D data to standard 2D format (C)
`imprep`	Set up rf pulses, imaging and voxel selection gradients (M)
`lpe`	Field of view size for phase encode axis (P)
`nf`	Number of FIDs (P)
`ni`	Number of increments in 1st indirectly detected dimension (P)
`nv2`	Number of phase encode steps for 2nd indirectly detected dim. (P)
`nv3`	Number of phase encode steps for 3rd indirectly detected dim. (P)
`seqcon`	Acquisition loop control (P)
`setloop`	Control arrayed and real-time looping (M)

nv2 — Number of phase encode steps for 2nd indirectly detected dimension

Description: The number of phase encode steps for the second indirectly detected dimension in a multidimensional imaging or CSI experiment.

In a 3D image, `nv2` controls the resolution in the third spatial dimension (`lpe2`). In a 2D (or higher) CSI experiment, `nv2` controls the second spatial dimension (`lpe2`). The lower level parameters `ni` and `nf` are automatically set each time a value of `nv` is entered, through the macro `setloop`, which uses the `seqcon` parameter to determine if the acquisition is standard or compressed in the dimension controlled by `nv2`, and appropriately sets either `ni` or `nf`. Because `nv2` is explicitly used in most imaging pulse sequences to specify the number of phase encode steps, the user should never directly set `ni` or `nf`, but instead set `nv2`, and let the software automatically assign `ni` and `nf`.

Related:

`flashc`	Convert compressed 2D data to standard 2D format (C)
`imprep`	Set up rf pulses, imaging and voxel selection gradients (M)
`lpe2`	Field of view size for 2nd phase-encode axis (P)
`nf`	Number of FIDs (P)
`ni`	Number of increments in 1st indirectly detected dimension (P)
`nv`	Number of phase encode steps for 1st indirectly detected dim. (P)
`nv3`	Number of phase encode steps for 3rd indirectly detected dim. (P)
`seqcon`	Acquisition loop control (P)
`setloop`	Set values for ni and nf to control arrayed and real-time looping (M)

nv3 — Number of phase encode steps for 3rd indirectly detected dimension

Description: The number of phase encode steps for the third indirectly detected dimension in a multidimensional experiment.

In a 3D CSI experiment (three spatial dimensions, one chemical shift dimension), `nv3` controls the third spatial dimension (`lpe3`). The lower level parameters `ni` and `nf` are set automatically each time a value of `nv3` is entered, through the macro `setloop`, which uses the `seqcon` parameter to determine if the acquisition is standard or compressed in the dimension controlled by `nv3`, and appropriately sets either `ni` or `nf`. Because `nv3` is explicitly used in most imaging pulse sequences to specify the number of phase encode steps, the user should never directly set `ni` or `nf`, but instead set `nv3`, and let the software automatically assign `ni` and `nf`.

Related:

`flashc`	Convert compressed 2D data to standard 2D format (C)
`imprep`	Set up rf pulses, imaging and voxel selection gradients (M)

lpe3	Field of view size for 3rd phase-encode axis (P)
nf	Number of FIDs (P)
ni	Number of increments in 1st indirectly detected dim. (P)
nv	Number of phase encode steps for 1st indirectly detected dim. (P)
nv2	Number of phase encode steps for 2nd indirectly detected dim. (P)
seqcon	Acquisition loop control (P)
setloop	Set values for ni and nf to control arrayed and real-time looping (M)

ticks **Number of trigger pulses for external gating**

Description: Specifies the number of trigger pulses the system waits before proceeding with pulse sequence execution. Most imaging pulse sequences include the pulse sequence function `xgate(ticks)` to synchronize the timing of pulse sequence execution with an external trigger event. Although any parameter name may be chosen by the pulse sequence programmer, `ticks` is predefined and available for this use.

Related:

hold	Post-trigger delay (P)
xgate	Load time counter (P)

Flag Parameters

ir **Inversion recovery mode**

Description: A flag used to turn on or off execution of an inversion-recovery pre-pulse in sequences that include this capability. Generally used to control an inversion-recovery block that uses the parameters `pi`, `pipat`, `ti`, and `tpwri`.

Values: `'y'` specifies inversion recovery mode; `'n'` specifies the mode is not used.

Related:

pi	Inversion pulse length (P)
pipat	Inversion pulse shape (P)
ti	Inversion recovery time (P)
tpwri	Inversion pulse power level (P)

mt **Magnetization transfer on/off**

Description: A flag used to turn on or off magnetization transfer preparation in sequences that include this capability.This parameter is generally used to control a magnetization transfer block that uses the parameters `pmt`, `mtpat`, and `mtpwr`.

Values: `'y'` means turn on magnetization transfer, `'n'` means turn it off.

Related:

mtpat	Magnetization transfer pulse rf shape (P)
mtpwr	Magnetization transfer pulse power level (P)
pmt	Magnetization pulse length (P)

pilot **Automatic sequence calculation**

Description: Specifies automatic or manual calculation of gradient refocusing levels in imaging pulse sequences. The automatic mode pulse sequence calculations are generally quite reliable, but it may sometimes be of interest to verify these calculations by arraying the parameters with `pilot` set to the manual mode. Operating at the extreme limits of the pulse sequence, such as ultra-short echo times, may also require some fine adjustment of refocusing gradient levels.

Values: 'y' sets the automatic mode that uses internally computed refocusing levels; 'n' sets the manual mode that bypasses internal calculations and directly uses the values found in the parameters gssr and gror.

Related:	gror	Read out dephasing gradient (P)
	gssf	Slice selection fractional refocusing (P)
	gssr	Slice selection refocusing gradient (P)

presat **Presaturation pulse execution on/off**

Description: Sets whether to turn on or off execution of a presaturation pulse in sequences that include this capability. This parameter is generally used to control a presaturation block that uses the parameters psat, satfrq, satpat, and satpwr.

Values: 'y' means turn on execution; 'n' means turn it off.

Related:	psat	Saturation pulse length (P)
	satfrq	Presaturation frequency (P)
	satpat	Presaturation pulse rf shape (P)
	satpwr	Saturation/presaturation pulse power level (P)

rfspoil **RF spoiling on/off**

Description: Sets whether to turn on or off rf spoiling in sequences that include this capability. This parameter is generally used to control an rf spoiling block in fast gradient echo sequences.

Values: 'y' means turn on rf spoiling; 'n' means turn it off.

Related:	rfphase	Phase angle (P)

ws **Water suppression on/off**

Description: Sets whether to turn on or off water suppression in sequences that include this capability.

Values: 'y' means turn on water suppression; 'n' means turn off water suppression or to specify additional characters in some pulse sequences that provide more than one water suppression technique.

Related:	wsfrq	Water suppression (P)

Acquisition Loop Control

Several special parameters common to all imaging experiments exist for providing information for automated setup or controlling pulse sequence execution. These are seqcon and the list parameters fliplist, patlist, plist, pwrlist, and sslist. The list parameters (covered in the next section) allow linking related parameters, such as p1, tpwr1, p1pat, together for use by automated setup macros.

seqcon **Acquisition loop control**

Description: Controls the status of various possible looping processes in most imaging sequences.

Values: 5-character string. The table on the right shows how each character position has “place value” and affects a different looping operation.

Position	*Loop*
First	Multiecho
Second	Multislice
Third	1st Phase Encode (2D)
Fourth	2nd Phase Encode (3D)
Fifth	3rd Phase Encode (4D)

The value of each character controls the type of loop used during pulse sequence execution for the corresponding sequence function (not all looping functions are present in most sequences):

- `n` specifies that this particular looping operation is *not* used in the sequence.
- `s` sets the looping operation to occur during the execution of pulse sequence generation in the host computer as a *standard* arrayed acquisition. Each pass through the loop generates a new *acode* set for execution in the acquisition computer, in turn returning a new data block in the FID file. A standard loop therefore lies outside the signal averaging (transient counter) loop. Parameter arrays and the implicit 2D loop are standard loops. The multiecho loop *cannot* be a standard loop because of the rapid timing restrictions normally associated with multiecho data acquisition.
- `c` sets the looping operation to occur dynamically in the acquisition computer, controlled by real-time pulse sequence variables. Each pass through a *compressed* loop generates a new data *trace* that is concatenated with data from previous passes through that loop to form a single data block in acquisition memory. Acquisition data memory must therefore be large enough to hold the total amount of data from any compressed acquisition loops before it is ultimately sent back to the host computer. Compressed loops lie inside the signal averaging loop.

Pulse sequence loop execution can be easily toggled between compressed and standard modes by changing the appropriate character field in `seqcon`. Changing the character field allows the same pulse sequence code to be used for different applications. For example, time course imaging studies are easily achieved by using a compressed phase encode mode, which completes each image before the next begins.

Examples: The following table lists some common `seqcon` settings:. e

nD	*seqcon*	*Application*
1	`'nnnnn'`	1D spectroscopy
2	`'ncsnn'`	2D imaging with compressed multislice, standard phase encode
2	`'nscnn'`	2D imaging with compressed phase encode and arrayed slice position (common in fast imaging sequences)
2	`'cssnn'`	2D imaging with compressed multiecho and arrayed slice position
2	`'ccsnn'`	2D imaging with compressed multiecho and multislice
3	`'nncsn'`	3D imaging with compressed phase encode loop in 2D, and standard phase encode loop in 3D

Related:	`nD`	Application dimension (P)
	`ne`	Number of echoes to be acquired (P)
	`ns`	Number of slices to be acquired (P)
	`nv`	Number of phase encode steps for 1st indirectly detected dim. (P)
	`tr`	Total repetition time of an acquisition sequence (P)

Pulse and Gradient List Parameters

The list parameters provide information used in automated computation of rf power levels, and slice or voxel selection gradient levels. Each of these parameters can be arrayed to form a series of parameter names or values (arraying these parameters does not cause arrayed data acquisition). Every list has an entry corresponding to each rf pulse in the sequence, providing sets of information about other parameters that are linked to each pulse event, such as power level, shaped pattern name, etc. All but the parameter `fliplist` are string parameters, and the entries in these string lists are the names of the parameters that describe the corresponding attribute (which can be inferred from the list parameter name itself). Examples are given for the parameter set found in the SEMS imaging sequence.

`fliplist` Flip angle list

Description: Contains a list of the desired flip angles for each rf pulse. Of the list parameters, `fliplist` is the only numerical parameter, the rest are string parameters. Each entry in `fliplist` specifies the target flip angle that the corresponding pulse should achieve in the sequence. The automated setup routines use this information, together with the pulse calibration database to compute the required power level. SEMS is a spin-echo imaging sequence, which typically uses 90° and 180 ° pulses, giving `fliplist=90,180`.

Related:	`imprep`	Set up rf pulses, imaging and voxel selection gradients (M)
	`patlist`	Pulse shape parameter list (P)
	`plist`	Pulse length parameter list (P)
	`pwrlist`	Pulse power level parameter list (P)
	`sslist`	Gradient parameter names list (P)

`p1` First pulse width

Description: Length of first pulse in the standard two-pulse sequence.

Values: On *MERCURY* systems: 0, 0.2 µs to 4095 µs. On *GEMINI 2000* systems: 0, 0.2 to 4095 µs, in 100-ns steps. On systems with a Data Acquisition Controller board: 0, 0.1 to 8190 µs, in 12.5-ns steps. On systems with Pulse Sequence Controller or Acquisition Controller boards: 0, 0.2 to 8190 µs, in 25-ns steps. On systems with Output boards: 0, 0.2 to 8190 µs, in 0.1-µs steps. (Refer to the `acquire` statement in the manual *VNMR User Programming* for a description of these boards.)

Related:	`p1`	Enter pulse width *p1* in degrees (C)

`patlist` Pulse shape parameter list

Description: Contains a list of the parameters that define the rf shapes used for each rf pulse in the sequence. The SEMS sequence uses two parameters to define the shapes used by the first and second rf pulses, `p1` and `p2`. These parameters are `p1pat` and `p2pat`, with `patlist='p1pat','p2pat'`.

`patlist` is a list of the shape file names, not the shape file names themselves (e.g., `patlist` would not be set to the explicit names `sinc`, `gauss`).

Related:	`fliplist`	Flip angle list (P)
	`imprep`	Set up rf pulses, imaging and voxel selection gradients (M)
	`plist`	Pulse length parameter list (P)
	`pwrlist`	Pulse power level parameter list (P)
	`sslist`	Gradient parameter names list (P)

`plist` Pulse length parameter list

Description: Contains a list of the rf pulse length parameter names used by the sequence For example, the SEMS sequence has a 90° pulse (`p1`) and a 180° refocusing pulse (`p2`), with `plist='p1','p2'`.

Related:	`fliplist`	Flip angle list (P)
	`imprep`	Set up rf pulses, imaging and voxel selection gradients (M)
	`patlist`	Pulse shape parameter list (P)
	`pwrlist`	Pulse power level parameter list (P)
	`sslist`	Conjugate gradient list (P)

`pwrlist` Pulse power level parameter list

Description: Contains a list of the rf power parameter names used for each pulse in the sequence. The SEMS sequence uses the parameters `tpwr1` and `tpwr2` to specify the power for the two corresponding pulses `p1` and `p2`, for example: `pwrlist='tpwr1','tpwr2'`.

Related:	`fliplist`	Standard flip angle list (P)
	`imprep`	Set up rf pulses, imaging and voxel selection gradients (M)
	`patlist`	Pulse shape parameter list (P)
	`plist`	Pulse length parameter list (P)
	`sslist`	Gradient parameter names list (P)

`sslist` Gradient parameter names list

Description: Contains a list of the gradient parameter names used for slice or voxel selection with each rf pulse in the sequence. The SEMS sequence uses the parameter `gss` to define the slice select gradient level for both rf pulses, giving `sslist='gss','gss'`. Some rf pulses in a sequence may not be slice or voxel selective, such as a presaturation or inversion pulses. The corresponding entry in `sslist` for these pulses should be `'n'`.

Another example is the ISIS sequence, which has a total of four pulses. The first three are voxel selective, with levels specified by the parameters `gvox1`, `gvox2`, and `gvox3`, as in `sslist='gvox1','gvox2','gvox3','n'`

Related:	`fliplist`	Standard flip angle list (P)
	`gss`	Slice selection gradient strength (P)
	`imprep`	Set up rf pulses, imaging and voxel selection gradients (M)
	`patlist`	Pulse shape parameter list (P)
	`plist`	Pulse length parameter list (P)
	`pwrlist`	Pulse power level parameter list (P)

Target Parameters

Each imaging and localized spectroscopy experiment contains a group of parameters that are used to hold information on a temporary basis during the planning of new imaging slices or spectroscopy voxels. These are called *target* parameters, because they are used to transfer positional and orientational values planned from an existing scout image to a new target experiment. Each of the normal parameters that describe positions, dimensions, and orientations has a corresponding target parameter, with a name that is formed by adding the prefix `t_`. For example, slice positions that are planned for a new target experiment are held in the parameter `t_pss`; orientations for a new target slice plane are held in the parameters `t_phi`, `t_psi`, and `t_theta`, etc.

Miscellaneous Parameters

This section lists miscellaneous parameters that do not belong in the previous categories.

appmode **Application mode**

Applicability: All systems except *GEMINI 2000*.

Description: Allows selection of specialized system applications modes, such as imaging, by setting the global parameters `sysmaclibpath`, `sysmenulibpath`, and `syshelppath`. For example, in `/vnmr/maclib` is a subdirectory `maclib.imaging` that contains macros used primarily with imaging applications. Similarly, in `/vnmr/menulib` is a subdirectory `menulib.imaging` for imaging-related menus. By separating the imaging macros and menus into subdirectories, access to imaging-specific macros and menus is more convenient. This separation also allows minor modifications to some macros and menus while retaining the names that are in common use or required by other VNMR commands.

The `dconi` menu illustrates how `appmode` works. In normal 2D spectroscopy operation (defined by setting `appmode='standard'`), the `dconi` menu displays a button labeled Peak that provides access to interactive 2D peak-picking. With `appmode='imaging'`, however, this button is labeled Mark instead and now performs the 1D or 2D `mark` function, which is more appropriate for imaging data. The `dconi` menu tailored for imaging is found in `menulib.imaging`, which is searched by VNMR before searching the `/vnmr/menulib` directory when `appmode` is set to `'imaging'`. The search order is `userdir+'/?'` followed by `vnmrsys/maclib`, `maclibpath`, `sysmaclibpath`, and then `/vnmr/maclib`.

The value of `appmode` can be set either by entering its value directly from the command line or by selecting the Setup button from the Main Menu and then clicking on the App Mode button. New applications modes can be added by creating the appropriate subdirectories in `/vnmr/maclib`, `/vnmr/menulib`, and `/vnmr/help`, and adding the desired applications mode name to the `_appmode` macro. Subdirectories should be named by adding the file extension .`appmodename` to the corresponding parent directory name (for example, `maclib.solids`, `menulib.automation`).

Values: `'standard'` sets standard application mode. `'imaging'` sets imaging application mode.

Related: `config` Display current configuration and possibly change it (M)

fn **Fourier number in directly detected dimension**

Description: Selects the Fourier number for the Fourier transformation along the directly detected dimension. This dimension is often referred to as the f_2 dimension in 2D data sets, the f_3 dimension in 3D data sets, etc.

Values: `'n'` or a number equal to a power of 2 (minimum is 32). If `fn` is not *entered* exactly as a power of 2, it is automatically rounded to the nearest higher power of 2 (e.g., setting `fn=32000` gives `fn=32768`). `fn` can be less than, equal to, or greater than `np`, the number of directly detected data points:

- If `fn` is less than `np`, only `fn` points are transformed.
- If `fn` is greater than `np`, `fn` minus `np` zeros are added to the data table ("zero-filling").
- If `fn='n'`, `fn` is automatically set to the power of 2 greater than or equal to `np`.

Related:

`fn1`	Fourier number in 1st indirectly detected dimension (P)
`fn2`	Fourier number in 2nd indirectly detected dimension (P)
`np`	Number of data points (P)

fn1 **Fourier number in 1st indirectly detected dimension**

Description: Selects the Fourier number for the Fourier transformation along the first indirectly detected dimension. This dimension is often referred to as the f_1 dimension of a multi-dimensional data set. The number of increments along this dimension is controlled by the parameter `ni`.

Values: `fn1` is set in a manner analogous to the parameter `fn`, with `np` being substituted by `2*ni`.

Related:

`fn`	Fourier number in directly detected dimension (P)
`fn2`	Fourier number in 2nd indirectly detected dimension (P)
`ni`	Number of increments in 1st indirectly detected dimension (P)
`np`	Number of data points (P)

homo **Homodecoupling control for first decoupler**

Applicability: All systems except *MERCURY* and *GEMINI 2000;* however, *MERCURY* and *GEMINI 2000* automatically use gated decoupling when `tn` and `dn` are both in the high band (i.e., if `tn` and `dn` is ^{1}H or ^{19}F, and `dm='y'`).

Description: Enables time-shared decoupling. Unlike the `dm`, `dmm`, and `hs` parameters, `homo` is not under "status" control. On systems with type 2 or 3 interface board (`apinterface=2` or `apinterface=3`), `homo` does not control any signal routing; the position of the relevant relays is controlled by whether homonuclear decoupling (`tn` equals `dn`) or heteronuclear decoupling (`tn` not equal to `dn`) is in effect.

Values: On UNITY*INOVA* and UNITY*plus*, the values are `'n'` or `'y'`, where:

- `'n'` specifies no gating.
- `'y'` specifies that the receiver is gated, which is done by controlling the observe L.O. (local oscillator) line. If `dm ='y'`, first decoupler rf, amplifier (blanked/unblanked), and preamplifier are gated. If `dm='n'`, no gating of these signals takes place. When `homo` is set to `'y'`, `dmm` should be set to `'c'` for continuous wave (CW) modulation.

On UNITY and VXR-S, the values are `'n'` or `'y'`, where:

- 'n' disables decoupler time-sharing, which is appropriate for heteronuclear decoupling or for cases in which the decoupler is off during acquisition.
- 'y' selects time-shared decoupling, which is appropriate for homonuclear decoupling in which the receiver is gated off when the decoupler is on. On systems with the type 1 interface board (apinterface=1), homo='y' also causes the decoupler signal to be combined with the observe signal before being sent to the probe.

Related:		
	apinterface	AP Interface board type (P)
	dn	Nucleus for first decoupler (P)
	homo2	Homodecoupling control for second decoupler (P)
	homo3	Homodecoupling control for third decoupler (P)
	tn	Nucleus for observe transmitter (P)

nD Application dimension

Description: Sets the number of spatial dimensions. nD is used in automated setup to specify the number of phase encode dimensions that must be computed.

Values: 1, 2, 3, or 4. nD is 2 in 2D imaging, and 3 in 3D imaging.

Related:		
	imprep	Set up rf pulses, imaging and voxel selection gradients (M)
	seqcon	Acquisition loop control (P)

petable Table name in tablib

Description: Specifies the name of a table in tablib. The table named by petable is normally used to control the phase encode (k-space) order during data acquisition in sequences that offer this capability. Sequences written to support external phase encode tables generally allow petable='n', in which case the phase encode order is computed internally in the conventional monotonic order. tabc, the routine that reorders data acquired in table order, also uses petable to obtain the name of the table to be used in the reordering process.

Related:		
	tabc	Convert data in table order to linear order (M)

presig Preamplifier signal level selection

Applicability: UNITY*INOVA* and UNITY*plus* imaging systems, or UNITY*INOVA* and UNITY*plus* spectrometers with selectable large-signal mode preamplifiers.

Description: Controls preamplifier signal level selection.

Values: 'h' signifies high-signal mode at the preamplifier. If the signal level is unusually high, this value provides increased signal handling capacity, at some reduction in signal-to-noise. This mechanism is separate from the receiver gain control, which should be optimized before changing presig.

'l' signifies low signal mode at the preamplifier. This value provides the best signal-to-noise performance and should be used in normal operation for low to moderate signal levels

'n' signifies not used. presig defaults to low-signal mode at the preamplifier if the hardware is present.

Related:		
	gain	Receiver gain (P)

rfcoil **RF pulse calibration identity**

Description: Specifies an entry in the pulsecal (pulse calibration) database. Information from pulsecal is used for automated computation of rf power levels.

Related: imprep Set up rf pulses, imaging and voxel selection gradients (M)
pulsecal Create, modify, or delete entry in pulsecal rf calibration file (M)

rfphase **Phase angle**

Description: Phase angle used for rf spoiling in sequences that include this capability.

Description: Number, in degrees.

Related: rfspoil RF spoiling on/off (P)

A.6 Image Browser Commands Not in VNMR

data_header_set **Create and set float header variables (C, not in VNMR)**

Syntax: data_header_set ('parname','command')

Description: Provides a way of creating and setting new "float" type header variables in images that have already been loaded in to Image Browser.

Arguments: parname is the header parameter name that is created (if it does not exist) in all selected images.

command is the command line sent to the UNIX shell by data_header_set. The standard input of command is a list of names of the selected images (in the order that the images were selected).

Examples: frame_select ('none',1,2,3)
data_header_set ('myparm','cat data')

In the previous example, the frame_select command selects frames 1, 2, and 3. Then data_header_set sets the header myparm in the first three images to the respective values of the three numbers in the data file.

See also: Chapter 4, "Image Browser,"

vol_extract **Extract one plane orientation (C, not in VNMR)**

Syntax: vol_extract (['xt'|'yz'|'xz'], first_slice [,last_slice [, incr]])

Description: Extracts one orientation of planes as selected by 'xy' (the default), 'xz', or 'yz'; used to process 3D data.

Arguments: first__slice extracts only that plane number.

last__slice extracts planes >=first_slice and <=last_slice.

incr is the increment between successive slices; it should be positive.

Related: vol_mip Extract one slice (C)

vol_mip **Extract one slice (C, not in VNMR)**

Syntax: vol_mip (['xy'|'yz'|'xz'], first_slice [,last_slice [, incr]])

Description: Extracts only one slice, which is the pixel-by-pixel maximum of all the slices that `vol_extract` would have extracted; used to process 3D data.

Arguments: `first__slice` extracts only that plane number.

`last__slice` extracts planes `>=first_slice` and `<=last_slice`.

`incr` is the increment between successive slices; it should be positive.

Related: `vol_extract` Extract one plane orientation(C)

Symbols

Numerics

A

B

C

D

F

G

H

I

J

L

M

N

W

X

Y

Z